

Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF499613; AAM19249.1; -;  
DR MGD; MGI:2179523; Fcrl3.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
KW Receptor.  
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Best Local Similarity 41.1%; Pred. No. 1.2e-25;  
Matches 76; Conservative 33; Mismatches 76; Indels 0; Gaps 0;  
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QY 70 LSEETNSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGEPFLF 129  
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QY 130 LRCHGWRNDVYKVIYKDGKALKYWENHNISITNATVEDSGTYCTGKWQLDYSEPL 189  
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QY 190 LNIIV 194  
Db 185 FRISL 189

RESULT 12

QY Q7YQJ5 PRELIMINARY; PRT; 372 AA.  
AC Q7YQJ5; DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE High affinity IGG Fc gamma receptor 1.  
GN FCGAMWARI.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Shiba; TISSUE=Cutaneous;  
RX MEDLINE=22777889; PubMed=12811428;  
RA Nakamura R., Sato Y., Takagi K., Sasaki N., Sawada J., Kitani S.,  
RA Teshima R.;  
RT "Presence and primary sequence of a high-affinity IGG receptor on  
RT canine mastocytoma (CM-MC) cells";  
RL Immunogenetics 55:271-274 (2003).  
DR EMBL; AB101519; BAC80263.1; -;  
KW Receptor.  
SQ SEQUENCE 372 AA; 42336 MW; BC04026CD198049D CRC64;  
Query Match 34.2%; Score 366.5; DB 6; Length 372;  
Best Local Similarity 39.1%; Pred. No. 2.2e-25;  
Matches 72; Conservative 34; Mismatches 77; Indels 1; Gaps 1;  
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QY 71 SEETNSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGEPFLF 130  
Db 63 TOTLTPRYIAAASVNDNGEYRCQTGLSVLSPIQGIHRDWLILQVSRVTEGEPLTL 122  
QY 131 RCHGWRNDVYKVIYKDGKALKYWENHNISITNATVEDSGTYCTGKWQLDYSEPL 190

RESULT 10

Q8SPW2 PRELIMINARY; PRT; 254 AA.  
AC Q8SPW2; DT 01-JUN-2002 (TREMBlrel. 21, Created)  
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Fc gamma receptor IIa.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheidae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Nomencluk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,  
RA Presta L.G.;  
RT "Binding of human IGG to cynomolgus FcR";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF485815; AAL92098.1; -;  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR PROSITE; PS00835; IG\_LIKE; 2.  
KW Receptor.  
SQ SEQUENCE 254 AA; 29120 MW; 11A48E6B3A34AF7B CRC64;  
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Best Local Similarity 42.2%; Pred. No. 7.2e-26;  
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QY 10 LLCVALLFFAPDGVLA--VPQPKVSLNPPWNRIFKGNVTLTCGNPFVSSSTKWFH 67  
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QY 68 GSISETNSLNINAKFEDSGEYKCOHQVNESEPVYLEVFSDDLQASAEVVMGEP 127  
Db 64 ESISSQTSYFFAAARVNSGEVRCOTSLTSLSDPVQLEVHIGWLLQAPRVVKEES 123  
QY 128 LFRCHGWRNDVYKVIYKDGKALKYWENHNISITNATVEDSGTYCTGKWQLDYSE 187  
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QY 188 EPLNITV 194  
Db 184 ETVNITI 190

RESULT 11

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DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Transmembrane receptor CD16-2.  
GN FCRL3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL; TISSUE=Liver;  
RA Mechetina L.V., Najakshin A.M., Alabyev B.Y., Chikaev N.A.,  
RA Tarantin A.V.;  
RT "Identification of CD16-2, a novel mouse receptor homologous to  
RT CD16/FcgrIII.";

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Db 123 RCHGWNKLVYVNFQNGTVLKFSPQNSEFTILKTLTHNGIYHCSA-MGKHRYESAGV 181
QY 191 NITV 194
Db 182 SITI 185

RESULT 13
Q8R2R4 PRELIMINARY; PRT; 249 AA.
AC Q8R2R4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN FCRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC027310; AAH27310.1; -.
DR MGI; MGI:2179523; Fcrl3.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 249 AA; 28372 MW; 740D6BE8E1536224 CRC64;

Query Match 34.0%; Score 365; DB 11; Length 249;
Best Local Similarity 41.1%; Pred. No. 1.8e-25;
Matches 76; Conservative 33; Mismatches 76; Indels 0; Gaps 0;

QY 10 LLCVALLFFAPDGVLPQPKVSLNPPWNRIFKGENVTLTCNGNNFFVSSTKWPH 69
Db 5 LLPTALVLTSGIQAGLQKAVNLDPKVRVLEDSVTLRCQGTFFSPDINSIKWPH 64
QY 70 LSEETNSLNIIVNAKPEDSGYKCOHQVNESEPVYLEVFSMDLLQASAEVVMGQ 129
Db 65 LIPHQDANYITQSAKVDSGMYRCQTALSTISDPVQLEVHMGWLLLTQTKWLFQEGDPIH 124
QY 130 LRCHGWRNDVYKVIYKDGKALKYENHNISITNATVEDSGTYCTGKWQLDYSE 189
Db 125 LRCHSWQNPVRKVTYSQNGKGYFENSELLIPKATHNDSGSYFCRGLIGNKNSAS 184
QY 190 LNITV 194
Db 185 FRISL 189

RESULT 14
Q9N2I6 PRELIMINARY; PRT; 249 AA.
AC Q9N2I6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD16.
GN CD16.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]_TaxID=9685;
RP SEQUENCE FROM N.A.
RA Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
Mikami T., Takahashi E.;

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RT "Molecular cloning and sequencing of the cDNA encoding the feline
Fc(gamma)RIIIA (CD16) homologue.";
RL Vet. Immunol. Immunopathol. 73:353-359(2000).
DR EMBL; AB025314; BAA92347.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
SQ SEQUENCE 249 AA; 27902 MW; 683528C68A7CAB7A CRC64;

Query Match 33.8%; Score 363; DB 6; Length 249;
Best Local Similarity 42.0%; Pred. No. 2.8e-25;
Matches 79; Conservative 25; Mismatches 80; Indels 4; Gaps 1;

QY 7 SPTLLCVALLFFAPDGVLPQPKVSLNPPWNRIFKGENVTLTCNGNNFFVSSTKWPH 66
Db 6 SPT---ALLLVASAGTRADLSKAMVLEPEWNRVLDGVILKCEGAYPPGDNSAQW 61
QY 67 NGSLSSETNSLNIIVNAKPEDSGYKCOHQVNESEPVYLEVFSMDLLQASAEVVMGQ 126
Db 62 NGSVIPHRAPSYSEIARSEDSEYKCOGTGLSEADPVQLEVHTGWLILQAPRWV 121
QY 127 PLFLRCHGWRNDVYKVIYKDGKALKYENHNISITNATVEDSGTYCTGKWQLDY 186
Db 122 TIQLRCHSWKNTVQKVQFQDGRGMFFHKNSDYIPKATSKHSGSYFCRGLIGN 181
QY 187 SEPLNITV 194
Db 182 SEAVNITV 189

RESULT 15
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AC Q9ES92;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fc gamma receptor II.
GN Fcgr3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Fossati J, Mack L., Boucrot E., Izui S.;
RT "Mouse Fc gamma RII: identification and characterization of a new
allele in C57BL/6 mice.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBSJ databases.
RN [2]_
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;
RX MEDLINE=22354663; PubMed=12466851;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AF197930; AAG28520.1; -.
DR EMBL; AK077227; BAC36696.1; -.
DR MGI; MGI:95500; Fcgr3.
DR GO; GO:0004872; Fc receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
KW Receptor.
SQ SEQUENCE 261 AA; 30098 MW; 9C8570E032F94730 CRC64;

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GenCore version 5.1.6  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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4	516	100.0	528	6	AX274969	AX274969 Sequence
5	516	100.0	560	6	BD264322	BD264322 Recombina
6	516	100.0	560	6	AX026805	AX026805 Sequence
7	516	100.0	591	6	AR175486	AR175486 Sequence
8	516	100.0	591	6	AX074293	AX074293 Sequence
9	516	100.0	591	6	AX074295	AX074295 Sequence
10	516	100.0	696	6	AX074290	AX074290 Sequence
11	516	100.0	696	6	AX074292	AX074292 Sequence
12	516	100.0	699	6	AR175483	AR175483 Sequence
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14	516	100.0	773	6	AR219964	AR219964 Sequence
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41	508	98.4	516	6	BD267592	BD267592 Crystalli
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ALIGNMENTS

RESULT 1  
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LOCUS AR175487 516 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 12 from patent US 6309832.  
ACCESSION AR175487  
VERSION AR175487.1 GI:17916786  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 516)  
AUTHORS Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.  
TITLE Method to detect IGE  
JOURNAL Patent: US 6309832-A 12 30-OCT-2001;  
FEATURES Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 2.2e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
AX074296 516 bp DNA linear PAT 06-FEB-2001
LOCUS
DEFINITION Sequence 10 from Patent WO0104310.
ACCESSION AX074296
VERSION AX074296.1 GI:12710483
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
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AUTHORS Weber E.R., Wood, K.V. and Hall, M.P.
TITLE Fc epsilon receptor-luminescence inducing protein chimeric nucleic
acid molecules, fusion proteins and uses thereof
JOURNAL Patent: WO 0104310-A 10 18-JAN-2001;
Heska Corporation (US); PROMEGA CORPORATION (US)
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CDS
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Best Local Similarity 100.0%; Pred. No. 2.2e-147;
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DB 181 GAAGACAGTGAGAAATACAAATGTCAGCACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
QY 241 CTGGAAGTCTTTCAGTGACTGGCTGCTCTTCAGGCCCTCTGCTGAGGTGGTGATGGAGGC 300
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QY 301 CAGCCCTCTTCTCAGTGCTCCATGTTGGAGAACCTGGAGTGTGAAGTGTGATCTAT 360
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QY 361 TATAAGGATGTGAAGCTCTCAAGTACTGGTATCAGAACCAACATCTCCATTACAAAT 420
DB 361 TATAAGGATGTGAAGCTCTCAAGTACTGGTATCAGAACCAACATCTCCATTACAAAT 420
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
DB 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

RESULT 3
AX074298 516 bp DNA linear PAT 06-FEB-2001
LOCUS
DEFINITION Sequence 12 from Patent WO0104310.
ACCESSION AX074298
VERSION AX074298.1 GI:12710485
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
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AUTHORS Weber E.R., Wood, K.V. and Hall, M.P.
TITLE Fc epsilon receptor-luminescence inducing protein chimeric nucleic
acid molecules, fusion proteins and uses thereof
JOURNAL Patent: WO 0104310-A 12 18-JAN-2001;
Heska Corporation (US); PROMEGA CORPORATION (US)
FEATURES
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ORIGIN
Query Match
Best Local Similarity 100.0%; Score 516; DB 6; Length 560;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGGTCCTCTTGAACCTCCTGAACTGGAATAGAAATATTTAAAGGAG 60
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QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
Db 70 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 129

QY 121 CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGATTTGAATATTTGTAATGCCAAATTT 180
Db 130 CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGATTTGAATATTTGTAATGCCAAATTT 189

QY 181 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAGTAAATGAGAGTGAACCTGTGTAC 240
Db 190 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAGTAAATGAGAGTGAACCTGTGTAC 249

QY 241 CTGGAAGTCTTTCAGTGAAGTCTGCTCTTTCAGGCTCTGCTGAGGTCGTGATGAGGGC 300
Db 250 CTGGAAGTCTTTCAGTGAAGTCTGCTCTTTCAGGCTCTGCTGAGGTCGTGATGAGGGC 309

QY 301 CAGCCCTCTTCTCAGTGCCTGCTCTTTCAGGCTCTGCTGAGGTCGTGATGAGGGC 360
Db 310 CAGCCCTCTTCTCAGTGCCTGCTCTTTCAGGCTCTGCTGAGGTCGTGATGAGGGC 369

QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGCTGATGAGAACCAACAATCTCCATTAACAAT 420
Db 370 TATAAGGATGGTGAAGTCTCAAGTACTGCTGATGAGAACCAACAATCTCCATTAACAAT 429

QY 421 GCCACAGTGAAGACAGTGAAGTCTCAAGTACTGCTGATGAGAACCAACAATCTCCATTAACAAT 480
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QY 481 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCT 516
Db 490 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCT 525

RESULT 7
AX026805 560 bp DNA linear PAT 16-SEP-2000
LOCUS
DEFINITION
Sequence 11 from Patent EP1006193.
ACCESSION
AX026805
VERSION
AX026805.1 GI:10187938
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
Recombinant soluble fc receptors
TITLE
Patent: EP 1006183-A 11 07-JUN-2000;
JOURNAL
MAX PLANCK GESELLSCHAFT (DE)
FEATURES
Location/Qualifiers
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ORIGIN
Query Match
Best Local Similarity 100.0%; Score 516; DB 6; Length 560;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
Db 70 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 129

QY 121 CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGATTTGAATATTTGTAATGCCAAATTT 180
Db 130 CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGATTTGAATATTTGTAATGCCAAATTT 189

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QY 241 CTGGAAGTCTTTCAGTGAAGTCTGCTCTTTCAGGCTCTGCTGAGGTCGTGATGAGGGC 300
Db 250 CTGGAAGTCTTTCAGTGAAGTCTGCTCTTTCAGGCTCTGCTGAGGTCGTGATGAGGGC 309

QY 301 CAGCCCTCTTCTCAGTGCCTGCTCTTTCAGGCTCTGCTGAGGTCGTGATGAGGGC 360
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QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGCTGATGAGAACCAACAATCTCCATTAACAAT 420
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QY 421 GCCACAGTGAAGACAGTGAAGTCTCAAGTACTGCTGATGAGAACCAACAATCTCCATTAACAAT 480
Db 430 GCCACAGTGAAGACAGTGAAGTCTCAAGTACTGCTGATGAGAACCAACAATCTCCATTAACAAT 489

QY 481 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCT 516
Db 490 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCT 525

RESULT 6
AX026805 560 bp DNA linear PAT 16-SEP-2000
LOCUS
DEFINITION
Sequence 11 from Patent EP1006193.
ACCESSION
AX026805
VERSION
AX026805.1 GI:10187938
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1
Recombinant soluble fc receptors
TITLE
Patent: EP 1006183-A 11 07-JUN-2000;
JOURNAL
MAX PLANCK GESELLSCHAFT (DE)
FEATURES
Location/Qualifiers
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ORIGIN
Query Match
Best Local Similarity 100.0%; Score 516; DB 6; Length 560;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
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QY 121 CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGATTTGAATATTTGTAATGCCAAATTT 180
Db 130 CACAATGGCAGCCTTTTCAGAGAGACAAATTCAGATTTGAATATTTGTAATGCCAAATTT 189

QY 181 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAGTAAATGAGAGTGAACCTGTGTAC 240
Db 190 GAAGACAGTGGAGAAATACAAATGTCAGACCAACAAGTAAATGAGAGTGAACCTGTGTAC 249

QY 241 CTGGAAGTCTTTCAGTGAAGTCTGCTCTTTCAGGCTCTGCTGAGGTCGTGATGAGGGC 300
Db 250 CTGGAAGTCTTTCAGTGAAGTCTGCTCTTTCAGGCTCTGCTGAGGTCGTGATGAGGGC 309

QY 301 CAGCCCTCTTCTCAGTGCCTGCTCTTTCAGGCTCTGCTGAGGTCGTGATGAGGGC 360
Db 310 CAGCCCTCTTCTCAGTGCCTGCTCTTTCAGGCTCTGCTGAGGTCGTGATGAGGGC 369

QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGCTGATGAGAACCAACAATCTCCATTAACAAT 420
Db 370 TATAAGGATGGTGAAGTCTCAAGTACTGCTGATGAGAACCAACAATCTCCATTAACAAT 429

QY 421 GCCACAGTGAAGACAGTGAAGTCTCAAGTACTGCTGATGAGAACCAACAATCTCCATTAACAAT 480
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QY 481 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCT 516
Db 490 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCT 525

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QY 301 CAGCCCTCTTCCTCAGTGGTCCATGTTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 360
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QY 361 TATAAGAGTGTGAAGTCTCAAGTACTGTTGAGAACTGGGATGTGTACAAAGTGTATCTAT 420
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QY 421 GCCACAGTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480
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QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
Db 556 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591

RESULT 8
AX074293
LOCUS AX074293 591 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 7 from Patent WO0104310.
ACCESSION AX074293
VERSION AX074293.1 GI:12710480
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Weber,E.R., Wood,K.V. and Hall,M.P.
TITLE Fc epsilon receptor-luminescence inducing protein chimeric nucleic
acid molecules, fusion proteins and uses thereof
JOURNAL Patent: WO 0104310-A 7 18-JAN-2001;
Heska Corporation (US) ; PROMEGA CORPORATION (US)
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ORIGIN
Query Match 100.0%; Score 516; DB 6; Length 591;
Best Local Similarity 100.0%; Pred No. 2.3e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGAGAG 60
Db 76 GTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGAGAG 135
QY 61 AATGTGACTCTTACATGTAAATGGGAACAAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
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QY 241 CTGGAAGTCTTCAGTGAAGTCTGCTCTCTCAGGCTCTGCTGAGGTGGTGTATGAGAGGC 300
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QY 301 CAGCCCTCTTCCTCAGTGGTCCATGTTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 360
Db 376 CAGCCCTCTTCCTCAGTGGTCCATGTTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 435
QY 361 TATAAGAGTGTGAAGTCTCAAGTACTGTTGAGAACTGGGATGTGTACAAAGTGTATCTAT 420
Db 436 TATAAGAGTGTGAAGTCTCAAGTACTGTTGAGAACTGGGATGTGTACAAAGTGTATCTAT 495
QY 421 GCCACAGTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480
Db 496 GCCACAGTGAAGACAGTGGAACTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 555
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
Db 556 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591

RESULT 9
AX074295/C
LOCUS AX074295 591 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 9 from Patent WO0104310.
ACCESSION AX074295
VERSION AX074295.1 GI:12710482
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Weber,E.R., Wood,K.V. and Hall,M.P.
TITLE Fc epsilon receptor-luminescence inducing protein chimeric nucleic
acid molecules, fusion proteins and uses thereof
JOURNAL Patent: WO 0104310-A 9 18-JAN-2001;
Heska Corporation (US) ; PROMEGA CORPORATION (US)
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ORIGIN
Query Match 100.0%; Score 516; DB 6; Length 591;
Best Local Similarity 100.0%; Pred No. 2.3e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTGTGAATATTTGAATGCCAAATTT 180
Db 396 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTGTGAATATTTGAATGCCAAATTT 337
QY 181 GAAGACAGTGGAGAAATCAAAATGTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
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Db      216 CAGCCCTCTCTCTCAGTGCTGGCTGCTCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 157
QY      361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 420
Db      156 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 97
QY      421 GCCACAGTTGAAGACAGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 480
Db      96 GCCACAGTTGAAGACAGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 37
QY      481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
Db      36 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 1

RESULT 10
AX074290
LOCUS      AX074290          696 bp      DNA      linear      PAT 06-FEB-2001
DEFINITION Sequence 4 from Patent WO0104310.
ACCESSION  AX074290
VERSION     AX074290.1  GI:12710477
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Weber, E.R., Wood, K.V. and Hall, M.P.
TITLE       Fc epsilon receptor-luminescence inducing protein chimeric nucleic
JOURNAL     acid molecules, fusion proteins and uses thereof
            Patent: WO 0104310-A 4 18-JAN-2001;
            Heska Corporation (US) ; PROMEGA CORPORATION (US)
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CDS
Query Match      100.0%; Score 516; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.4e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  GTCCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGAG 60
Db      1  GTCCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGAG 60
QY      61  AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
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QY      121  CACAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTCGAATATTTGAATGCCAAATTT 180
Db      121  CACAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTCGAATATTTGAATGCCAAATTT 180
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Db      181  GAAGACAGTGGAGAATACAAATGTTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240
QY      241  CTGGAAGTCTTCAGTGACTGGCTGCTCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 300
Db      241  CTGGAAGTCTTCAGTGACTGGCTGCTCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 300
QY      301  CAGCCCTCTCTCTCAGTGCTGGCTGCTCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 360
Db      301  CAGCCCTCTCTCTCAGTGCTGGCTGCTCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 360
QY      361  TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 420
Db      361  TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 420
QY      421  GCCACAGTTGAAGACAGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 480
Db      421  GCCACAGTTGAAGACAGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 480
QY      481  GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516
Db      481  GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

RESULT 11
AX074292/c
LOCUS      AX074292          696 bp      DNA      linear      PAT 06-FEB-2001
DEFINITION Sequence 6 from Patent WO0104310.
ACCESSION  AX074292
VERSION     AX074292.1  GI:12710479
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Weber, E.R., Wood, K.V. and Hall, M.P.
TITLE       Fc epsilon receptor-luminescence inducing protein chimeric nucleic
JOURNAL     acid molecules, fusion proteins and uses thereof
            Patent: WO 0104310-A 6 18-JAN-2001;
            Heska Corporation (US) ; PROMEGA CORPORATION (US)
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Query Match      100.0%; Score 516; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 2.4e-147;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  GTCCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGAG 60
Db      596  GTCCCTCAGAAACCTAAGGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAGAG 637
QY      61  AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
Db      636  AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 577
QY      121  CACAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTCGAATATTTGAATGCCAAATTT 180
Db      576  CACAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTCGAATATTTGAATGCCAAATTT 517
QY      181  GAAGACAGTGGAGAATACAAATGTTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240
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QY      241  CTGGAAGTCTTCAGTGACTGGCTGCTCTCTCAGGCTCTGCTGAGGTGGTATGAGGGC 300
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QY 481 GAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 516  
Db 216 GAGTCTGAGCCCTCAACATTACTGTATATAAAGCT 181

RESULT 12  
AR175483  
LOCUS AR175483 699 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 7 from patent US 6309832.  
ACCESSION AR175483  
VERSION AR175483.1 GI:17916782  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
AUTHORS Unclassified.  
TITLE 1 (bases 1 to 699)  
JOURNAL Frank,G.R., Porter,J.P., Rushlow,K.E. and Wasson,D.L.  
METHOD Method to detect Ige  
PATENT Patent: US 6309832-A 7 30-OCT-2001;  
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ORIGIN  
Query Match 100.0%; Score 516; DB 6; Length 699;  
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Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 CTGGAAGTCTTCAAGTGTGCTCTCTTCAGGCTCTCTGCTGAGGTGGTGTGAGGGC 300  
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QY 301 CAGCCCTCTTCTCAGGTGCGATGGTGTGAGGAACCTGGATGTACAGGTGATCTAT 360  
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RESULT 13  
E07699  
LOCUS E07699 713 bp RNA linear PAT 29-SEP-1997  
DEFINITION cDNA encoding human soluble Fc epsilon RI alpha chain.  
ACCESSION E07699  
VERSION E07699.1 GI:2175833  
KEYWORDS JP 1994169776-A/1.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
JOURNAL 1 (bases 1 to 713)  
COMMENT PRODUCTION OF SOLUBLE HUMAN FcEPSILONRIALPHA CHAIN  
PATENT: JP 1994169776-A 1 21-JUN-1994;  
OS RA TOMOYASU, GREEN CROSS CORP:THE  
PN OS Homo sapiens (human)  
PD JP 1994169776-A/1  
PF 21-JUN-1994 JP 1993208217  
PR 29-JUL-1993 JP 92P 229227  
PI 04-AUG-1992 JP 92P 229227  
PC RA TOMOYASU, NAITO YUKITSUGU, HIRAMA MINORU  
CC C12N15/13,C12N5/10,C12P21/02;  
CC strandedness: Double;  
CC topology: Linear;  
CC hypothetical: No;  
CC anti-sense: No; Location/Qualifiers  
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Query Match 100.0%; Score 516; DB 6; Length 713;  
Best Local Similarity 100.0%; Pred. No. 2.4e-147;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 GAAGACAGTGGAGATACAAATGTCAGACCAACAGTTAATGAGAGTGAACCTGTGAC 240  
Db 375 GAAGACAGTGGAGATACAAATGTCAGACCAACAGTTAATGAGAGTGAACCTGTGAC 434  
QY 241 CTGGAAGTCTTCAAGTGTGCTCTCTTCAGGCTCTCTGCTGAGGTGGTGTGAGGGC 300  
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555 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 614  
Qy 421 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480  
615 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 674  
Qy 481 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516  
675 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 710  
RESULT 14  
AR219964  
LOCUS AR219964  
DEFINITION Sequence 6 from patent US 6423512.  
ACCESSION AR219964  
VERSION AR219964.1 GI:2324331  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 773)  
AUTHORS Digan,M.E., Lake,P. and Gram,H.  
TITLE Fusion polypeptides  
JOURNAL Patent: US 6423512-A 6 23-JUL-2002;  
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Best Local Similarity 100.0%; Pred. No. 2.5e-147;  
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436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 495  
Qy 421 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480  
496 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 555  
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556 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591  
Search completed: October 10, 2004, 16:11:56  
Job time : 2246.88 secs

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Qy 421 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480  
615 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 674  
Qy 481 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516  
675 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 710  
RESULT 14  
AR219964  
LOCUS AR219964  
DEFINITION Sequence 6 from patent US 6423512.  
ACCESSION AR219964  
VERSION AR219964.1 GI:2324331  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 773)  
AUTHORS Digan,M.E., Lake,P. and Gram,H.  
TITLE Fusion polypeptides  
JOURNAL Patent: US 6423512-A 6 23-JUL-2002;  
FEATURES  
source Location/Qualifiers  
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Query Match 100.0%; Score 516; DB 6; Length 773;  
Best Local Similarity 100.0%; Pred. No. 2.5e-147;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTCCCTCAGAACCTAAGTCTCCTGACCCCTCATGGAATAGAAATATTTAAAGGAG 60  
76 GTCCCTCAGAACCTAAGTCTCCTGACCCCTCATGGAATAGAAATATTTAAAGGAG 135  
Qy 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120  
136 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 195  
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Qy 181 GAAGACAGTGGAGAAATACAAATGTGAGAGAGACAAATTTCAAGTTTGAATATTTGAATGCCAAATTT 240  
256 GAAGACAGTGGAGAAATACAAATGTGAGAGAGACAAATTTCAAGTTTGAATATTTGAATGCCAAATTT 315  
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316 CTGGAAGTCTTCAAGTACTGGTCTCTCTCAGGCTCTGCTGAGGTGGTGTGATGGAGGC 375  
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376 CAGCCCTCTTCTCAGTGGCCATGGTTGGAGAACTGGGATGTGTACAAGTGATCTAT 435  
Qy 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 495  
Qy 421 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480  
496 GCCACAGTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 555  
Qy 481 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 516  
556 GAGTCTGAGCCCTCAACATTACTGTATAAAAGCT 591  
Search completed: October 10, 2004, 16:11:56  
Job time : 2246.88 secs



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OM nucleic - nucleic search, using sw model

Run on: October 8, 2004, 15:03:47 ; Search time 250.898 Seconds  
(without alignments)  
8736.904 Million cell updates/sec

Title: US-10-763-400-12  
Perfect score: 516  
Sequence: 1 gccctcgaaacctaaagt.....acattactgtaataaaagct 516

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124095041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneseqn1990s: \*  
3: geneseqn2000s: \*  
4: geneseqn2001as: \*  
5: geneseqn2001bs: \*  
6: geneseqn2002s: \*  
7: geneseqn2003as: \*  
8: geneseqn2003bs: \*  
9: geneseqn2003cs: \*  
10: geneseqn2004s: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	516	100.0	516	3	AAA27302 Human nhf
2	516	100.0	516	5	Aaf24917 DNA encod
3	516	100.0	516	5	Aaf24918 Complemen
4	516	100.0	528	3	AAA27301 Human Fce
5	516	100.0	528	4	Aah47768 Nucleotid
6	516	100.0	570	3	AAA27472 Recombina
7	516	100.0	591	5	Aaf24916 Complemen
8	516	100.0	591	5	Aaf24915 DNA encod
9	516	100.0	696	5	Aaf24914 Complemen
10	516	100.0	696	5	Aaf24913 Nucleotid
11	516	100.0	713	2	Aaq55969 Human dii
12	516	100.0	773	2	Aav20402 Human IGE
13	516	100.0	773	6	Abs52959 Human cdn
14	516	100.0	774	4	Aaf97964 Human imm
15	516	100.0	851	2	Aaq27267 Human fce
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21	516	100.0	1198	2	Aav36343 cDNA enco
22	516	100.0	1198	3	AAA34813 Human ade
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25	516	100.0	1198	5	Aaf24912 Complemen
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28	516	100.0	1198	7	ABZ96629 Human hig
29	516	100.0	1198	9	ADB85535 Human imm
30	516	100.0	1198	9	Aaf24929 Fc epsilo
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33	516	100.0	2193	5	Aaf24926 Fc epsilo
34	516	100.0	2193	5	Aaf24923 Complemen
35	516	100.0	2268	5	Aaf24921 Complemen
36	516	100.0	2268	5	Aaf24920 Nucleotid
37	516	100.0	2955	2	Aav20404 Plasmid R
38	516	100.0	2955	6	AB552957 Human cdn
39	516	100.0	21742	3	AAA34816 Human ade
40	516	100.0	21742	3	Aaf20938 Human hig
41	516	100.0	21742	7	ABZ96632 Human hig
42	516	100.0	117608	7	ABZ97129 Human rec
43	516	100.0	117609	3	Aaf21435 Human rec
44	514.4	99.7	1199	2	AAQ14736 Human Fc(
45	512.8	99.4	1193	2	AAQ04644 Encodes a

ALIGNMENTS

RESULT 1  
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ID AAA27302 standard; cDNA; 516 BP.  
XX  
AC AAA27302;  
DT 01-AUG-2000 (first entry)  
XX Human nhFcpsilonRIalpha 1-516 gene.  
DE Protein co-ordinate data; nhFcpsilonRIalpha 1-516; FcR;  
KW FcpsilonRIalpha 1-516; antibody Fc receptor; allergy;  
KW anaphylactic shock; ss.  
XX Homo sapiens.  
FH Key Location/Qualifiers  
CDS 1..516  
FT /\*tag= a  
FT /product= "nhFcpsilonRIalpha 1-516"  
FT /partial  
XX WO200026246-A2.  
XX 11-MAY-2000.  
XX 05-NOV-1999; 99WO-US026203.  
XX 05-NOV-1999; 98US-0107219P.  
XX (HESK-) HESKA CORP.  
XX (NOUN ) UNIV NORTHWESTERN.  
XX Jardetsky TS, Garman SC, Kinet J;  
XX WPI; 2000-365577/31.  
XX P-PSDB; AAY94211.  
XX Three-dimensional model comprising an extracellular domain of a human  
XX high affinity Fc epsilon receptor alpha chain protein, useful for  
XX identifying inhibitors and useful mutans.  
XX Example 6; Page 461; 463pp; English.  
XX The present sequence is the human FcpsilonRIalpha 1-516 gene (also known  
XX as nhFcpsilonRIalpha 1-516). Along with either the FcpsilonRI beta

CC and/or gamma subunits, the protein produced from this gene is involved in  
 CC mast cell activation and the triggering of allergic reactions and  
 CC anaphylactic shock. The protein can be used to identify useful mutants  
 CC and inhibitors, which can then be used in the detection of  
 CC (susceptibility to) allergies and in protecting animals from these  
 CC allergies

SQ Sequence 516 BP; 155 A; 107 C; 124 G; 130 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 516; DB 3; Length 516;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-148; Indels 0; Gaps 0;  
 Matches 516; Conservative 0; Mismatches 0;  
 QY 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60  
 DB 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60  
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 DB 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAGTGAACCTGTGTAC 240  
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 DB 361 TATAGGATGGTGAAGCTCTCAAGTCTGCTGAGTGTGAGAACCAACATCTCCATTACAAAT 420  
 QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480  
 DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480  
 QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516  
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## RESULT 2

AAF24917

ID AAF24917 standard; DNA; 516 BP.

XX AC AAF24917;

XX 30-APR-2001 (first entry)

XX DT DNA encoding Fc epsilon receptor alpha-chain secretable protein.

XX DE Fc epsilon receptor; Fc epsilon receptor; immunoglobulin E; IgE; atopic disease;

XX KW luminescence inducing protein; allergy; hyper IgE syndrome;

XX KW internal parasite infection; B cell neoplasia; ss.

XX OS Homo sapiens.

XX XX WO200104310-A1.

XX PN 18-JAN-2001.

XX PD 13-JUL-2000; 2000WO-US019070.

XX PF 13-JUL-1999; 99US-0143612P.

XX PR

PR 02-MAR-2000; 2000US-0186412P.

XX (HESK-) HESKA CORP.

PA (PROM-) PROMEGA CORP.

XX PI Weber ER, Wood KV, Hall MP;

XX WIPI; 2001-103082/11.

XX P-PSDB; AAB31587.

XX A fusion protein, comprising an Fc epsilon receptor domain and a  
 PT luminescence inducing protein domain that induces a LP substrate to emit  
 PT light when contacted with the LP domain, useful for detecting  
 PT immunoglobulin (Ig) E.

PS Claim 17; Page 66-67; 105pp; English.

XX The present sequence encodes a secretable form of a human Fc epsilon  
 CC receptor (Fc epsilonR) alpha-chain. The Fc epsilonR protein binds to  
 CC immunoglobulin (Ig) E. The Fc epsilonR domain is used to produce a fusion  
 CC protein, which also comprises a luminescence inducing protein domain that  
 CC induces a substrate to emit light when contacted with the luminescence  
 CC inducing protein domain. The fusion protein may be used to detect IgE. It  
 CC may also be used to identify a compound capable of inhibiting Fc epsilonR  
 CC protein activity. IgE antibody production is indicative of diseases such  
 CC as allergies, atopic disease, hyper IgE syndrome, internal parasite  
 CC infections and B cell neoplasia. Detection of IgE production in an animal  
 CC following therapy is indicative of the efficacy of the treatment, for  
 CC example when using treatments intended to disrupt IgE production

XX Sequence 516 BP; 155 A; 107 C; 124 G; 130 T; 0 U; 0 Other;

Query Match 100.0%; Score 516; DB 5; Length 516;

Best Local Similarity 100.0%; Pred. No. 2.1e-148;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60

DB 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGGTTC 120

DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCCACCAATGGTTC 120

QY 121 CACAATGCGAGCTTTTCAAGAGACAAATTCAAAGTTTGAATATTGGAATGCCAAATTT 180

DB 121 CACAATGCGAGCTTTTCAAGAGACAAATTCAAAGTTTGAATATTGGAATGCCAAATTT 180

QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAGTGAACCTGTGTAC 240

DB 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTTAATGAGTGAACCTGTGTAC 240

QY 241 CTGGAAGTCTTCAAGTCTGCTCTCTCAGGCCCTCTGCTGAGGTGGTGGAGGGC 300

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DB 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGAGTGTACAAAGGTGATCTAT 360

QY 361 TATAGGATGGTGAAGCTCTCAAGTCTGCTGAGTGTGAGAACCAACATCTCCATTACAAAT 420

DB 361 TATAGGATGGTGAAGCTCTCAAGTCTGCTGAGTGTGAGAACCAACATCTCCATTACAAAT 420

QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480

DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480

QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516

DB 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516

RESULT 3  
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ID AAF24918 standard; DNA; 516 BP.  
XX  
AC AAF24918;  
XX  
AT 30-APR-2001 (first entry)  
XX  
DE Complement of Fc epsilon receptor alpha-chain secretable protein DNA.  
XX  
XX Fc epsilon receptor; Fc epsilonR; immunoglobulin E; IgE; atopic disease;  
KW luminescence inducing protein; allergy; hyper IgE syndrome;  
KW internal parasite infection; B cell neoplasia; ss.  
XX  
XX Homo sapiens.  
OS  
XX WO200104310-A1.  
PN  
XX 18-JAN-2001.  
PD  
XX 13-JUL-2000; 2000WO-US019070.  
PF  
XX 13-JUL-1999; 99US-0143612P.  
PR  
XX 02-MAR-2000; 2000US-0186412P.  
PR  
XX (HESK-) HESKA CORP.  
XX (PROM-) PROMEGA CORP.  
PA  
XX Weber ER, Wood KV, Hall MP;  
PI  
XX WPI; 2001-103082/11.  
DR  
XX  
XX A fusion protein, comprising an Fc epsilon receptor domain and a  
PT luminescence inducing protein domain that induces a LP substrate to emit  
PT light when contacted with the LP domain, useful for detecting  
PT immunoglobulin (Ig) E.  
PT  
XX  
XX Example; Page 67-68; 105pp; English.  
PS  
XX  
XX The present sequence represents a secretable form of a human Fc epsilon  
CC receptor (Fc epsilonR) alpha-chain. The Fc epsilonR protein binds to  
CC immunoglobulin (Ig) E. The Fc epsilonR domain is used to produce a fusion  
CC protein, which also comprises a luminescence inducing protein domain that  
CC induces a substrate to emit light when contacted with the luminescence  
CC inducing protein domain. The fusion protein may be used to detect IgE. It  
CC may also be used to identify a compound capable of inhibiting Fc epsilonR  
CC protein activity. IgE antibody production is indicative of diseases such  
CC as allergies, atopic disease, hyper IgE syndrome, internal parasite  
CC infections and B cell neoplasia. Detection of IgE production in an animal  
CC following therapy is indicative of the efficacy of the treatment, for  
CC example when using treatments intended to disrupt IgE production  
XX  
XX Sequence 516 BP; 130 A; 124 C; 107 G; 155 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 516; DB 5; Length 516;  
Best Local Similarity 100.0%; Pred. No. 2.1e-148;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTCCTCAGAAACCTTAAGGTCCTCTTGAACCCCTCCATGGAATAGATATTAAAGAGAG 60  
DB 516 GTCCTCAGAAACCTTAAGGTCCTCTTGAACCCCTCCATGGAATAGATATTAAAGAGAG 457  
QY 61 AATGTGACTCTTACATGCTATGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120  
DB 456 AATGTGACTCTTACATGCTATGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 397  
QY 121 CACAATGGAGCCCTTTCAGAGACACAAATTCAGTTTGAATTTGTAATGCCAAATTT 180  
DB 396 CACAATGGAGCCCTTTCAGAGACACAAATTCAGTTTGAATTTGTAATGCCAAATTT 337  
QY 181 GAAGACAGTGGAGAAATCAAAATGTGACACCAACCAAGTTAATGAGAGTGAACCTGTCTAC 240  
DB 336 GAAGACAGTGGAGAAATCAAAATGTGACACCAACCAAGTTAATGAGAGTGAACCTGTCTAC 277

QY 241 CTGGAAGTCTTCAGTGAAGTGGTGGTCTCTTCAGGGCTCTGTCAGGTGGTGGTGGGCG 300  
DB 276 CTGGAAGTCTTCAGTGAAGTGGTGGTGGTCTCTTCAGGGCTCTGTCAGGTGGTGGGCG 217  
QY 301 CAGCCCTCTCTCTCAGGTGGCATGGTGGAGAACTGGATGTGTACAAAGTGATCTAT 360  
DB 216 CAGCCCTCTCTCTCAGGTGGCATGGTGGAGAACTGGATGTGTACAAAGTGATCTAT 157  
QY 361 TATAAGAGTGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 420  
DB 156 TATAAGAGTGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTACAAAT 97  
QY 421 GCCACAGTTGAACACAGTGGAACTTACTACTGACGGCAAAAGTGTGGCAGCTGGACTAT 480  
DB 96 GCCACAGTTGAACACAGTGGAACTTACTACTGACGGCAAAAGTGTGGCAGCTGGACTAT 37  
QY 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAAGCT 516  
DB 36 GAGTCTGAGCCCTCAACATTACTGTAAATAAAAGCT 1  
RESULT 4  
AAA27301  
ID AAA27301 standard; cDNA; 528 BP.  
XX  
XX AAA27301;  
AC  
XX  
DT 01-AUG-2000 (first entry)  
XX  
XX Human Fc epsilonR alpha 1-528 gene.  
DE  
XX  
KW Protein co-ordinate data; nhFc epsilonR alpha 1-528;  
KW Fc epsilonR alpha 1-528; FcR; antibody Fc receptor; allergy;  
KW anaphylactic shock; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Location/Qualifiers  
FT Key 1..528  
FT CDS /\*tag= a  
FT /\*product= "Fc epsilonR alpha 1-528"  
FT /\*partial  
XX  
XX WO200026246-A2.  
XX  
XX 11-MAY-2000.  
XX  
XX 05-NOV-1999; 99WO-US026203.  
XX  
XX 05-NOV-1998; 98US-0107219P.  
XX  
XX (HESK-) HESKA CORP.  
XX (NOUN) UNIV NORTHWESTERN.  
XX  
XX Jardetzky TS, Garman SC, Kinet J;  
XX  
XX WPI; 2000-365577/31.  
XX P-PSDB; AAY94210.  
XX  
XX Three-dimensional model comprising an extracellular domain of a human  
PT high affinity Fc epsilon receptor alpha chain protein, useful for  
PT identifying inhibitors and useful muteins.  
XX  
XX Disclosure; Page 459-460; 463pp; English.  
PS  
XX  
XX The present sequence is the human Fc epsilonR alpha 1-528 gene (also known  
CC as nhFc epsilonR alpha 1-528). Along with either the Fc epsilonR beta  
CC and/or gamma subunits, the protein produced from this gene is involved in  
CC mast cell activation and the triggering of allergic reactions and  
CC anaphylactic shock. The protein can be used to identify useful muteins  
CC and inhibitors, which can then be used in the detection of  
CC (susceptibility to) allergies and in protecting animals from these

CC allergies  
SQ Sequence 528 BP; 158 A; 110 C; 129 G; 131 T; 0 U; 0 Other;  
Query Match 100.0%; Score 516; DB 3; Length 528;  
Best Local Similarity 100.0%; Pred. No. 2.1e-148;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 60  
DB 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 60  
QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTTCCACCAATGTTTC 120  
DB 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTTCCACCAATGTTTC 120  
QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGCCAAATTT 180  
DB 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGCCAAATTT 180  
QY 181 GAAGACAGTGAGAAATACAAATGTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
DB 181 GAAGACAGTGAGAAATACAAATGTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTGAGGTGGTGTGGAGGGC 300  
DB 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTGAGGTGGTGTGGAGGGC 300  
QY 301 CAGCCCTCTTCTCAGTGGCCTATGTTGGAGGAACCTGGATGTGTACAAAGTGAATCTAT 360  
DB 301 CAGCCCTCTTCTCAGTGGCCTATGTTGGAGGAACCTGGATGTGTACAAAGTGAATCTAT 360  
QY 361 TATAAGGATGGTGAAGCTCTCAAGTCTCTGATGAGAACCAACATCTCCATTACAAAT 420  
DB 361 TATAAGGATGGTGAAGCTCTCAAGTCTCTGATGAGAACCAACATCTCCATTACAAAT 420  
QY 421 GCCACAGTTGAAGACAGTGAACCTCTACTCTGACGGGCAAGTGTGGAGCTGGACTAT 480  
DB 421 GCCACAGTTGAAGACAGTGAACCTCTACTCTGACGGGCAAGTGTGGAGCTGGACTAT 480  
QY 481 GAGTCTGAGCCCTCAACATTTACTGTAAATAAAGCT 516  
DB 481 GAGTCTGAGCCCTCAACATTTACTGTAAATAAAGCT 516  
RESULT 5  
AAH47768  
ID AAH47768 standard; DNA; 528 BP.  
XX AC AAH47768;  
XX DT 07-JAN-2002 (first entry)  
XX DE Nucleotide sequence of nhFcpsilonRlaphal-528 molecule.  
XX KW Antibody receptor protein; FcpsilonRlapha protein; immunoglobulin; IgE;  
XX MW muain; allergy; protein co-ordinate; ds.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
XX CDS 1..528 a  
XX FT /tag= a  
XX FT /product= "FcpsilonRlaphal-176"  
XX FN WO200169253-A2.  
XX PP 20-SEP-2001.  
XX PR 14-MAR-2001; 2001WO-US008586.  
XX PR 15-MAR-2000; 2000US-0189853P.  
XX PR

(HESK-) HESKA CORP.  
(NOUN ) UNIV NORTHWESTERN.  
Jardetzky TS, Garman SC, Wurzburg BA, Kinet J;  
WPI; 2001-511403/70.  
P-PSDB; AAG65597.  
Three dimensional models of complexes between antibody receptor proteins and antibodies used to identify modulators of antibody/receptor binding.  
PS Disclosure; Page 209-210; 213pp; English.  
XX The invention relates to three dimensional models of complexes between antibody receptor proteins, especially FcpsilonRlapha proteins, and antibodies, especially Fc-Cepsilon3/Cepsilon4 regions of immunoglobulin (Ig) E antibodies. The models are used to identify an inhibitor of the selective binding between a FcpsilonRlapha protein and an IgE antibody. The model identifies crystal contacts between a FcpsilonRlapha protein and an Fc-Cepsilon3/Cepsilon4 region of an IgE antibody. A mutin that binds to an Fc domain of an antibody (the mutin has improved function (improved stability, increased affinity for an Fc domain of an antibody, altered substrate specificity, increased affinity for an Fc domain of an antibody, altered substrate specificity, and increased solubility) compared to a protein comprising a defined amino acid sequence given in the specification) is used; to protect an animal from an allergy; detect an allergy in an animal; and to enhance the performance of an IgE binding assay. The present sequence represents the nucleotide sequence of a nhFcpsilonRlaphal-528 molecule encoding a nhFcpsilonRlaphal-176 protein  
SQ Sequence 528 BP; 158 A; 110 C; 129 G; 131 T; 0 U; 0 Other;  
Query Match 100.0%; Score 516; DB 4; Length 528;  
Best Local Similarity 100.0%; Pred. No. 2.1e-148;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 60  
DB 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 60  
QY 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTTCCACCAATGTTTC 120  
DB 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTGAAGTCAGTTCCACCAATGTTTC 120  
QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGCCAAATTT 180  
DB 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGCCAAATTT 180  
QY 181 GAAGACAGTGAGAAATACAAATGTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
DB 181 GAAGACAGTGAGAAATACAAATGTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
QY 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTGAGGTGGTGTGGAGGGC 300  
DB 241 CTGGAAGTCTTTCAGTGAAGTCTCTCTTTCAGGCTCTCTGAGGTGGTGTGGAGGGC 300  
QY 301 CAGCCCTCTTCTCAGTGGCCTATGTTGGAGGAACCTGGATGTGTACAAAGTGAATCTAT 360  
DB 301 CAGCCCTCTTCTCAGTGGCCTATGTTGGAGGAACCTGGATGTGTACAAAGTGAATCTAT 360  
QY 361 TATAAGGATGGTGAAGCTCTCAAGTCTCTGATGAGAACCAACATCTCCATTACAAAT 420  
DB 361 TATAAGGATGGTGAAGCTCTCAAGTCTCTGATGAGAACCAACATCTCCATTACAAAT 420  
QY 421 GCCACAGTTGAAGACAGTGAACCTCTACTCTGACGGGCAAGTGTGGAGCTGGACTAT 480  
DB 421 GCCACAGTTGAAGACAGTGAACCTCTACTCTGACGGGCAAGTGTGGAGCTGGACTAT 480  
QY 481 GAGTCTGAGCCCTCAACATTTACTGTAAATAAAGCT 516  
DB 481 GAGTCTGAGCCCTCAACATTTACTGTAAATAAAGCT 516



CC protein domain. The fusion protein may be used to detect IGE. It may also  
 CC be used to identify a compound capable of inhibiting FcεpsilonR protein  
 CC activity. IGE antibody production is indicative of diseases such as  
 CC allergies, atopic disease, hyper IGE syndrome, internal parasite  
 CC infections and B cell neoplasia. Detection of IGE production in an animal  
 CC following therapy is indicative of the efficacy of the treatment, for  
 CC example when using treatments intended to disrupt IGE production  
 XX  
 SQ Sequence 591 BP; 154 A; 141 C; 129 G; 167 T; 0 U; 0 Other;

Query Match 100.0%; Score 516; DB 5; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-148;  
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60  
 DB 516 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 457  
 QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120  
 DB 456 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 397  
 QY 121 CACAATGCGCCCTTCAGAGAGACAAATTCAGTTTGAATTTGAATGTCGCAATTT 180  
 DB 396 CACAATGCGCCCTTCAGAGAGACAAATTCAGTTTGAATTTGAATGTCGCAATTT 337  
 QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
 DB 336 GAAGACAGTGGAGAAATACAAATGTGAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 277  
 QY 241 CTGGAAGTCCTTCAAGTCTGCTCTTCAAGTCTGCTCTGAGGCTCTCTGAGGCTGATGGAGGC 300  
 DB 276 CTGGAAGTCCTTCAAGTCTGCTCTTCAAGTCTGCTCTGAGGCTCTCTGAGGCTGATGGAGGC 217  
 QY 301 CAGCCCTCTTCTCAGTGGTGGTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 360  
 DB 216 CAGCCCTCTTCTCAGTGGTGGTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 157  
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTCTGATGATGAGAACCAACATCTCCATTACAAAT 420  
 DB 156 TATAAGGATGGTGAAGCTCTCAAGTCTGATGATGAGAACCAACATCTCCATTACAAAT 97  
 QY 421 GCCACAGTTGAAGACAGTGAAGTCTTACTGTACGGGCAAGTGTGGAGCTGGACTAT 480  
 DB 96 GCCACAGTTGAAGACAGTGAAGTCTTACTGTACGGGCAAGTGTGGAGCTGGACTAT 37  
 QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516  
 DB 36 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 1

## RESULT 8

AAF24915

ID AAF24915 standard; DNA; 591 BP.

XX AAF24915;

XX AC

XX AC

DT 30-APR-2001 (first entry)

XX XX

DE DNA encoding Fc epsilon receptor alpha-chain extracellular domain.

XX Fc epsilon receptor; FcεpsilonR; immunoglobulin E; IGE; atopic disease;

KW luminescence inducing protein; allergy; hyper IGE syndrome;

KW internal parasite infection; B cell neoplasia; ss.

XX Homo sapiens.

OS Homo sapiens.

XX WO200104310-A1.

XX 18-JAN-2001.

XX 13-JUL-2000; 2000WO-US019070.

XX 13-JUL-2000; 2000WO-US019070.

XX 13-JUL-2000; 2000WO-US019070.

XX 13-JUL-2000; 2000WO-US019070.

XX 13-JUL-2000; 2000WO-US019070.

XX 13-JUL-2000; 2000WO-US019070.

PR 13-JUL-1999; 99US-0143612P.  
 PR 02-MAR-2000; 2000US-0186412P.  
 XX (HESK-) HESKA CORP.  
 PA (PROM-) PROMEGA CORP.  
 XX Weber ER, Wood KV, Hall MP;  
 XX WPI; 2001-103082/11.  
 DR P-PSDB; AAB31586.  
 XX A fusion protein, comprising an Fc epsilon receptor domain and a  
 PT luminescence inducing protein domain that induces a LP substrate to emit  
 PT light when contacted with the LP domain, useful for detecting  
 PT immunoglobulin (Ig) E.  
 XX Claim 17; Page 64-65; 105pp; English.  
 XX The present sequence encodes the extracellular domain of a human Fc  
 CC epsilon receptor (FcεpsilonR) alpha-chain. The FcεpsilonR protein binds  
 CC to immunoglobulin (Ig) E. The FcεpsilonR domain is used to produce a  
 CC fusion protein, which also comprises a luminescence inducing protein  
 CC domain that induces a substrate to emit light when contacted with the  
 CC luminescence inducing protein domain. The fusion protein may be used to  
 CC detect IGE. It may also be used to identify a compound capable of  
 CC inhibiting FcεpsilonR protein activity. IGE antibody production is  
 CC indicative of diseases such as allergies, atopic disease, hyper IGE  
 CC syndrome, internal parasite infections and B cell neoplasia. Detection of  
 CC IGE production in an animal following therapy is indicative of the  
 CC efficacy of the treatment, for example when using treatments intended to  
 CC disrupt IGE production  
 XX  
 SQ Sequence 591 BP; 167 A; 129 C; 141 G; 154 T; 0 U; 0 Other;

Query Match 100.0%; Score 516; DB 5; Length 591;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-148;  
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 60  
 DB 76 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGAATAGATATTAAAGGAGAG 135  
 QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120  
 DB 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 195  
 QY 121 CACAATGCGCCCTTCAGAGAGACAAATTCAGTTTGAATTTGAATGTCGCAATTT 180  
 DB 196 CACAATGCGCCCTTCAGAGAGACAAATTCAGTTTGAATTTGAATGTCGCAATTT 255  
 QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
 DB 256 GAAGACAGTGGAGAAATACAAATGTGAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 315  
 QY 241 CTGGAAGTCTTCAAGTCTGCTCTTCAAGTCTGCTCTGAGGCTCTCTGAGGCTGATGGAGGC 300  
 DB 316 CTGGAAGTCTTCAAGTCTGCTCTTCAAGTCTGCTCTGAGGCTCTCTGAGGCTGATGGAGGC 375  
 QY 301 CAGCCCTCTTCTCAGTGGTGGTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 360  
 DB 376 CAGCCCTCTTCTCAGTGGTGGTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 435  
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTCTGATGATGAGAACCAACATCTCCATTACAAAT 420  
 DB 436 TATAAGGATGGTGAAGCTCTCAAGTCTGATGATGAGAACCAACATCTCCATTACAAAT 495  
 QY 421 GCCACAGTTGAAGACAGTGAAGTCTTACTGTACGGGCAAGTGTGGAGCTGGACTAT 480  
 DB 496 GCCACAGTTGAAGACAGTGAAGTCTTACTGTACGGGCAAGTGTGGAGCTGGACTAT 555  
 QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516  
 DB 556 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 591

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RESULT 9
AAF24914/c
ID AAF24914 standard; DNA; 696 BP.
XX
XX
AC AAF24914;
XX
XX 30-APR-2001 (first entry)
XX
XX Complement sequence of Fc epsilon receptor alpha-chain mature protein.
XX
XX Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia; ss.
XX
XX Homo sapiens.
XX
XX WO200104310-A1.
XX
XX 18-JAN-2001.
XX
XX 13-JUL-2000; 2000WO-US019070.
XX
XX 13-JUL-1999; 99US-0143612P.
XX
XX 02-MAR-2000; 2000US-0186412P.
XX
XX (HESK-) HESKA CORP.
XX
XX (PROM-) PROMEGA CORP.
XX
XX Weber ER, Wood KV, Hall MP;
XX
XX WPI; 2001-103082/11.
XX
XX A fusion protein, comprising an Fc epsilon receptor domain and a
XX luminescence inducing protein domain that induces a LP substrate to emit
XX light when contacted with the LP domain, useful for detecting
XX immunoglobulin (Ig) E.
XX
XX Example; Page 63; 105pp; English.
XX
XX The present sequence represents the complement sequence of a
XX polynucleotide encoding human Fc epsilon receptor (FcepsilonR) alpha-
XX chain mature protein, that binds to immunoglobulin (Ig) E. The
XX FcepsilonR domain is used to produce a fusion protein, which also
XX comprises a luminescence inducing protein domain that induces a substrate
XX to emit light when contacted with the luminescence inducing protein
XX domain. The fusion protein may be used to detect IgE. It may also be used
XX to identify a compound capable of inhibiting FcepsilonR protein activity.
XX IgE antibody production is indicative of diseases such as allergies,
XX atopic disease, hyper IgE syndrome, internal parasite infections and B
XX cell neoplasia. Detection of IgE production in an animal following
XX therapy is indicative of the efficacy of the treatment, for example when
XX using treatments intended to disrupt IgE production
XX
XX SQ Sequence 696 BP; 179 A; 159 C; 150 G; 208 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 516; DB 5; Length 696;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-148;
XX Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGATATTTAAGGAG 60
XX
XX 696 GTCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGATATTTAAGGAG 637
XX
XX 61 AATGTACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120
XX
XX 636 AATGTACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 577
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XX 121 CACAATGGCAGCCCTTCAGAGAGACAAATTCAGTTTGAATATGGAATGCCAAATTT 180
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XX 576 CACAATGGCAGCCCTTCAGAGAGACAAATTCAGTTTGAATATGGAATGCCAAATTT 517
XX
181 GAAGACAGTGGAGATACAAATGTCAGACCAACCAAGTTTAATGAGAGTGAACCTGTGTAC 240
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CC atopic disease, hyper IGE syndrome, internal parasite infections and B  
 CC cell neoplasia. Detection of IGE production in an animal following  
 CC therapy is indicative of the efficacy of the treatment, for example when  
 CC using treatments intended to disrupt IGE production

XX Sequence 696 BP; 208 A; 150 C; 159 G; 179 T; 0 U; 0 Other;

Query Match 100.0%; Score 516; DB 5; Length 696;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-148;  
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 60  
 Db 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 60

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120  
 Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120

QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAAAATTT 180  
 Db 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAAAATTT 180

QY 181 GAAGACAGTGGAGATACAAATGTCAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
 Db 181 GAAGACAGTGGAGATACAAATGTCAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 240

QY 241 CTGGAAGTCTTCACTGACTGCTCTCTTCAGGCCCTCTCTGAGGTGGTGGAGGGC 300  
 Db 241 CTGGAAGTCTTCACTGACTGCTCTCTTCAGGCCCTCTCTGAGGTGGTGGAGGGC 300

QY 301 CAGCCCTCTTCTCAGGTGCCATGTTGGAGGAACTGGGATGTGTACAAAGTGTAT 360  
 Db 301 CAGCCCTCTTCTCAGGTGCCATGTTGGAGGAACTGGGATGTGTACAAAGTGTAT 360

QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
 Db 361 TATAAGGATGGTGAAGTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420

QY 421 GCCACAGTTGAAGACAGTGAACCTACTGTACGGGCAAAAGTGGCAGCTGGACTAT 480  
 Db 421 GCCACAGTTGAAGACAGTGAACCTACTGTACGGGCAAAAGTGGCAGCTGGACTAT 480

QY 481 GAGTCTCAGCCCTCAACATTACTGTAAATAAAGCT 516  
 Db 481 GAGTCTCAGCCCTCAACATTACTGTAAATAAAGCT 516

RESULT 11  
 AAQ55969  
 ID AAQ55969 standard; DNA; 713 BP.  
 XX AAQ55969;  
 AC AAQ55969;  
 XX 25-MAR-2003 (revised)  
 DT 12-SEP-1994 (first entry)  
 XX Human dihydrofolate reductase (DHFR) gene.  
 XX Dihydrofolate reductase; DHFR; marker; transformation; ss.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 XX CDS 120..713  
 FT /\*tag= a  
 FT /product= "Dihydrofolate reductase."  
 XX WO9403599-A1.  
 XX 17-FEB-1994.  
 XX 03-AUG-1993; 93WO-JP001085.

XX 04-AUG-1992; 92JP-00229227.  
 PR 10-AUG-1992; 92JP-00213002.  
 PR 08-OCT-1992; 92JP-00270513.  
 PR 08-OCT-1992; 92JP-00270514.  
 PR 08-OCT-1992; 92JP-00270515.  
 XX (GREC ) GREEN CROSS CORP.  
 PA Ra C, Naito K, Hirama M, Okumura K;  
 PI WPI; 1994-065687/08.  
 DR P-PSDB; AAR45778.  
 XX Antiallergic peptide derived from high-affinity immunoglobulin E receptor  
 PT - binds to human immunoglobulin E to block allergic reactions at source.  
 XX Disclosure; Page 24-25; 37pp; Japanese.  
 XX The dihydrofolate reductase (DHFR) gene was used in the construction of a  
 CC vector as a selectable marker. The resulting vector was used to transform  
 CC DHFR-deficient CHO cells. (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 713 BP; 202 A; 166 C; 163 G; 182 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 516; DB 2; Length 713;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-148;  
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 60  
 Db 135 GTCCCTCAGAACCTTAAGTCTCCTTGAACCTCCATGGAATAGAATATTTAAAGGAGAG 254

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAAAATGGTTC 120  
 Db 255 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAAAATGGTTC 314

QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAAAATTT 180  
 Db 315 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTTGAATGCAAAATTT 374

QY 181 GAAGACAGTGGAGATACAAATGTCAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
 Db 375 GAAGACAGTGGAGATACAAATGTCAGCACCACAAAGTTAATGAGAGTGAACCTGTGTAC 434

QY 241 CTGGAAGTCTTCACTGACTGCTCTCTTCAGGCCCTCTCTGAGGTGGTGGAGGGC 300  
 Db 435 CTGGAAGTCTTCACTGACTGCTCTCTTCAGGCCCTCTCTGAGGTGGTGGAGGGC 494

QY 301 CAGCCCTCTTCTCAGGTGCCATGTTGGAGGAACTGGGATGTGTACAAAGTGTATCTAT 360  
 Db 495 CAGCCCTCTTCTCAGGTGCCATGTTGGAGGAACTGGGATGTGTACAAAGTGTATCTAT 554

QY 361 TATAAGGATGGTGAAGTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
 Db 555 TATAAGGATGGTGAAGTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 614

QY 421 GCCACAGTTGAAGACAGTGGAACTACTGTACGGGCAAAAGTGGCAGCTGGACTAT 480  
 Db 615 GCCACAGTTGAAGACAGTGGAACTACTGTACGGGCAAAAGTGGCAGCTGGACTAT 674

QY 481 GAGTCTCAGCCCTCAACATTACTGTAAATAAAGCT 516  
 Db 675 GAGTCTCAGCCCTCAACATTACTGTAAATAAAGCT 710

RESULT 12  
 AAV20402  
 ID AAV20402 standard; DNA; 773 BP.  
 XX AAV20402;  
 AC AAV20402;  
 XX 20-JUL-1998 (first entry)



XX	Human IgE receptor Fc-epsilon-RI alpha chain DNA.
XX	Fc-epsilon RI alpha chain; IgE receptor; human serum albumin;
XX	fusion protein; allergy; atopic dermatitis; asthma; urticaria; hay fever;
XX	eczema; anaphylaxis; gene therapy; diagnosis; transgenic animal; ds.
OS	Homo sapiens.
XX	Key Location/Qualifiers
FFH	sig_peptide 1..75
FTT	mat_peptide /*tag= a
FTT	76..773
FTT	/*tag= b
XX	WO9804718-A1.
PN	05-FEB-1998.
XX	25-JUL-1997; 97WO-EF004066.
PPF	26-JUL-1996; 96US-00690216.
PR	(NOVS ) NOVARTIS AG.
PA	Digan ME, Lake P, Gram H;
XX	WPI; 1998-130705/12.
XX	P-PSDB; AAW48094.
XX	New fusion polypeptide for, e.g. diagnosing allergies - comprises
XX	immunoglobulin E-binding domain fused to human serum albumin.
PT	Disclosure; Page 56; 77pp; English.
XX	This nucleotide sequence codes the dominant form of full-length native
CC	human IgE receptor Fc-epsilon RI alpha chain (see AAW48094). A claimed
CC	fusion protein (FP) comprises an IGE binding domain fused to at least one
CC	human serum albumin (HSA) component (see AAW38095), optionally via a
CC	peptide linker, and is especially a dimeric FP (see AAW48096) comprising
CC	HSA fused, at each of its N- and C-termini, to the extracellular domain
CC	(i.e. mature protein) of Fc-epsilon RI alpha chain. Also claimed are:
CC	nucleic acids encoding the FP; a vector; a process for preparing the FP;
CC	a method of performing gene therapy in humans that comprises removing
CC	somatic cells from a patient, genetically modifying them in culture by
CC	insertion of a polynucleotide that encodes the FP, and reintroducing the
CC	modified cells into the patient so that the FP is expressed by the cells
CC	of the patient; and use of the FP in an in vitro diagnostic assay to
CC	determine the level of IGE or auto-antibodies to Fc epsilon RI in a
CC	sample. The products can be used in the prevention and/or treatment of
CC	IGE-mediated allergic diseases and related disorders such as atopic
CC	dermatitis, atopic asthma, chronic urticaria, hayfever and eczema.
CC	Compared with using IGE binding domain alone, the FP has a longer serum
CC	life, and thus greater activity, without a loss of ability to bind serum
CC	IGE or circulating auto-antibodies
XX	Sequence 773 BP; 220 A; 173 C; 176 G; 204 T; 0 U; 0 Other;
XX	Query Match 100.0%; Score 516; DB 2; Length 773;
XX	Best Local Similarity 100.0%; Pred. No. 2.6e-148;
XX	Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GTCCCTCAGAACCTTAAGTCTCTTGAAACCTTCATGGAATAGAAATTTAAAGGAGAG 60
Db	76 GTCCCTCAGAACCTTAAGTCTCTTGAAACCTTCATGGAATAGAAATTTAAAGGAGAG 135
Qy	61 AATGTGACTTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120
Db	136 AATGTGACTTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAATGGTTC 195
Qy	121 CACAAATGCGACCTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGTCACCAAAATTT 180

XX

PS PS Disclosure; Fig 13; 49pp; English.

XX

The invention relates to a new fusion polypeptide or its pharmaceutically acceptable salt comprises at least one IgE-binding domain fused to at least one human serum albumin (HSA) component, where the IgE-binding domain is the sequence (a) defined residues Val26-Leu204 of the protein sequence appearing as ABG32801, or a truncation at the carboxy terminus by 1-12 amino acids. Also included are: (1) a fusion polypeptide defined by residues Val26-Leu978 of the protein appearing as ABG32803; (2) a polynucleotide sequence encoding the fusion protein; (3) a host cell transformed with the polynucleotide; (4) a method of preparing the fusion protein comprising transforming a host cell with a vector comprising a polynucleotide encoding the fusion polypeptide, expressing the fusion polypeptide in the cell, and recovering the fusion polypeptide from the host cell, optionally in the form of its salt; and (5) a vector for expressing a polynucleotide sequence encoding a fusion polypeptide of formula (I), (II), (III), (IV), or (V) or its salts (R<sub>1</sub>-L-R<sub>2</sub> (I), R<sub>2</sub>-L-R<sub>1</sub> (II), R<sub>1</sub>-L-R<sub>2</sub>-L-R<sub>1</sub> (III), R<sub>1</sub>-L-R<sub>1</sub>-L-R<sub>2</sub> (IV), R<sub>2</sub>-L-R<sub>1</sub>-L-R<sub>1</sub> (V)), where R<sub>1</sub> = the polypeptide (a) or its truncation at the carboxy terminus by 1-12 amino acids and R<sub>2</sub> = a polypeptide selected from the sequence defined by residues Asp25-Leu609 the human HSA sequence appearing as ABG32802, or its truncation at the carboxy terminus by 1-10 amino acids and L = independently a chemical bond, where the vector is PXMT3-Pla-HAS-Rla). The compositions and methods of the present invention are useful for the prevention and treatment of systemic allergy and other IgE-receptor-mediated disorders such as atopic dermatitis, atopic asthma and chronic urticaria. The IgE-binding polypeptide have a more prolonged effective serum life, more improved clinical utility in the treatment of allergy, as well as improved activity in a more efficient and cost-effective manner. The present sequence encodes the human IgE receptor Fcεpsilon1α used to make the fusion protein of the invention

Sequence 773 BP; 220 A; 172 C; 177 G; 204 T; 0 U; 0 Other;

Query Match 100.0%; Score 516; DB 6; Length 773;  
Best Local Similarity 100.0%; Pred. No. 2.6e-148;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAGGTCCTTGAACCTCCATGGAATAGAATATTAAAGGAGAG 60  
DB 76 GTCCCTCAGAACCTTAGGTCCTTGAACCTCCATGGAATAGAATATTAAAGGAGAG 135  
QY 61 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120  
DB 136 AATGTGACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 195  
QY 121 CACAATGGGACCTTTTTCAGAGAGACAAATTCGAATTTGAATTTGAATGCAAAATTT 180  
DB 196 CACAATGGGACCTTTTTCAGAGAGACAAATTCGAATTTGAATTTGAATGCAAAATTT 255  
QY 181 GAGACAGTGGGAATACAAATTCAGCACCACAAATTAATGAGAGTGAACCTGTGTAC 240  
DB 256 GAGACAGTGGGAATACAAATTCAGCACCACAAATTAATGAGAGTGAACCTGTGTAC 315  
QY 241 CTGGAAGTCTTTCAGTGAAGTGGTCTTTCAGGCTCTGCTGAGGTGGTGTGAGGGC 300  
DB 316 CTGGAAGTCTTTCAGTGAAGTGGTCTTTCAGGCTCTGCTGAGGTGGTGTGAGGGC 375  
QY 301 CAGCCCTCTTCTCAGGTGGCCTGTTGGAGGAACCTGGGATGTGACAGGTGATCTAT 360  
DB 376 CAGCCCTCTTCTCAGGTGGCCTGTTGGAGGAACCTGGGATGTGACAGGTGATCTAT 435  
QY 361 TATAAGGATGGTGAAGTCTTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAT 420  
DB 436 TATAAGGATGGTGAAGTCTTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAT 495  
QY 421 GCACAGTTGAGACAGTGAACCTTACTACTGTACGGGCAAAAGTGTGGCAGTGAATAT 480  
DB 496 GCACAGTTGAGACAGTGAACCTTACTACTGTACGGGCAAAAGTGTGGCAGTGAATAT 555  
QY 481 GAGTCTGAGCCCTCAACATTTACTGTAATAAAGCT 516

Db

556 GAGCTGTAGCCCTCAACATTACTGTATAAAGCT 591

RESULT 14

AAF97964

ID AAF97964 standard; cDNA; 774 BP.

XX

AC AAF97964;

XX

DT 19-JUN-2001 (first entry)

XX

DE Human immunoglobulin E receptor I alpha subunit coding sequence.

XX

KW Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;  
single nucleotide polymorphism; SNP; allele specific oligonucleotide;  
immunoassay; detection; ss.

XX

OS Homo sapiens.

XX

PN WO200111010-A2.

XX

PD 15-FEB-2001.

XX

PF 02-AUG-2000; 2000WO-US021097.

XX

PR 09-AUG-1999; 99US-0147860P.

XX

(GENA-) GENAISSANCE PHARM INC.

XX

PI Chew A, Denton RR, Duda A, Klien SE, Lanz EM, Nandabalan K;  
Stephens JC;

XX

DR WPI; 2001-202766/20.

XX

P-PSDB; AAB74667.

XX

PT New polynucleotide for gene therapy, comprises nucleotide polymorphisms  
in the immunoglobulin E receptor I alpha subunit gene.

XX

PS Claim 7; Fig 2; 99pp; English.

XX

The present invention describes an isolated polynucleotide (I) comprising a nucleotide sequence (S) which is a polymorphic variant of a reference sequence for the human immunoglobulin E receptor I alpha subunit (IGERA) gene or its fragment. The polymorphic variant comprises at least one polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9, PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide 251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at a position corresponding to nucleotide 530. (I) can be used in gene therapy. (I) is useful for therapeutic purposes. A polypeptide (II) encoded by (I) is useful in drug screening assays and in assays to measure the binding affinity of one or more candidate drugs targeting (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from solution and also reacts with (II) on Western or immunoblots of polyacrylamide gels on membrane supports or substrates. (III) is also useful in immunoassays to detect (II) in biological samples. AAF97965 to AAF9840 represent IGERA allele specific oligonucleotide probes; AAF98097 to AAF98140 represent IGERA gene polymorphism detection primers; and AAF98141 to AAF98180 represent IGERA gene PCR primers which are used in the exemplification of the present invention. The present sequence encodes the human IGERA protein used in the present invention

XX

SQ Sequence 774 BP; 221 A; 172 C; 177 G; 204 T; 0 U; 0 Other;

Query Match 100.0%; Score 516; DB 4; Length 774;  
Best Local Similarity 100.0%; Pred. No. 2.6e-148;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GTCCCTCAGAACCTTAGGTCCTTGAACCTCCATGGAATAGAATATTAAAGGAGAG 60  
76 GTCCCTCAGAACCTTAGGTCCTTGAACCTCCATGGAATAGAATATTAAAGGAGAG 135

DB

QY 61 AATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 120  
 DB 136 AATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 195  
 QY 121 CACAATGCGAGCCTTTTCAAGAGACAAATTCAGATTTGAATTTGATGCAATTT 180  
 DB 196 CACAATGCGAGCCTTTTCAAGAGACAAATTCAGATTTGAATTTGATGCAATTT 255  
 QY 181 GAAGCAGTGGAGATCAAAATGTCAGACCAACCAAGTTAATGAGATGAACCTGTGTAC 240  
 DB 256 GAAGCAGTGGAGATCAAAATGTCAGACCAACCAAGTTAATGAGATGAACCTGTGTAC 315  
 QY 241 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGCCTCTCTGAGGTGGTGTGAGGGC 300  
 DB 316 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGCCTCTCTGAGGTGGTGTGAGGGC 375  
 QY 301 CAGCCCTCTTCTCAGTGCCATGGTGGAGAACTGGGATGTTACAAAGGTGACTAT 360  
 DB 376 CAGCCCTCTTCTCAGTGCCATGGTGGAGAACTGGGATGTTACAAAGGTGACTAT 435  
 QY 361 TATAAGGATGTGAAGCTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 420  
 DB 436 TATAAGGATGTGAAGCTCTCAAGTACTGATGATGAGAACCAACATCTCCATTACAAAT 495  
 QY 421 GCCACAGTTGAAGCAGTGGAACTTACTGTTACGGGCAAGTGGGAGTGGACTAT 480  
 DB 496 GCCACAGTTGAAGCAGTGGAACTTACTGTTACGGGCAAGTGGGAGTGGACTAT 555  
 QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516  
 DB 556 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 591

## RESULT 15

AAQ27267

ID AAQ27267 standard; DNA; 851 BP.

XX AC AAQ27267;

XX DT 25-MAR-2003 (revised)

XX DT 02-FEB-1993 (first entry)

XX DE Human FcERI alpha-subunit and IL-2 hybrid gene.

XX DE High affinity Fc immunoglobulin E receptor; IgE; antibody; interleukin-2;

XX KW histamine release; allergy; ss.

XX OS Homo sapiens.

XX FH Key

XX FT CDS

XX FT Location/Qualifiers

XX FT 107..806

XX FT /\*tag= a

XX FT /product= "alpha-subunit\_IL-2"

XX PN EP499112-A1.

XX PD 19-AUG-1992.

XX PF 03-FEB-1992; 92EP-00101732.

XX PR 11-FEB-1991; 91US-00653936.

XX XX (HOFF ) HOFFMANN LA ROCHE &amp; CO AG F.

XX PI Chizzonite RA, Hakimi J, Kochan JP;

XX DR WPI; 1992-277871/34.

XX PT Monoclonal antibodies bind to alpha sub-unit of Fc IgE receptor - for

XX PT treatment and prevention of IgE induced allergic diseases, also for

XX PT measuring alpha sub-unit and IgE levels in biological fluids.

XX PS Disclosure; Page 6; 30pp; English.

XX

This is a preferred hybrid gene for use in generating the monoclonal antibodies of the invention. The gene contains nucleotide sequence 121-710 of the human FcERI alpha-subunit to which nucleotides 876-1016 of the IL-2 receptor (the cytoplasmic and transmembrane regions) have been fused. (The nucleotide sequence of the human alpha-subunit is published in Nucleic Acid Research, 16(8):3584 (1989); the nucleotide sequence of the human p55 IL-2 receptor is published in Nature, 311:631 (1984). Cytoplasmic and transmembrane regions from receptors other IL-2 receptor can be used. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 851 BP; 241 A; 197 C; 204 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 516; DB 2; Length 851;

Best Local Similarity 100.0%; Pred. No. 2.7e-148; Indels 0; Gaps 0;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG 60

DB 182 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGATAATTTAAAGGAGAG 241

QY 61 AATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 120

DB 242 AATGTGACTCTTACATGTAATGGAACAAATTTCTTTGAAGTCAGTTCCACCAAAATGGTTC 301

QY 121 CACAATGCGAGCCTTTTCAAGAGACAAATTCAGATTTGAATTTGATGCAATTT 180

DB 302 CACAATGCGAGCCTTTTCAAGAGACAAATTCAGATTTGAATTTGATGCAATTT 361

QY 181 GAAGCAGTGGAGATCAAAATGTCAGACCAACCAAGTTAATGAGATGAACCTGTGTAC 240

DB 362 GAAGCAGTGGAGATCAAAATGTCAGACCAACCAAGTTAATGAGATGAACCTGTGTAC 421

QY 241 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGCCTCTCTGAGGTGGTGTGAGGGC 300

DB 422 CTGGAAGTCTTCAAGTACTGCTCTCTTCAAGCCTCTCTGAGGTGGTGTGAGGGC 481

QY 301 CAGCCCTCTTCTCAGTGCCATGGTGGAGAACTGGGATGTTACAAAGGTGACTAT 360

DB 482 CAGCCCTCTTCTCAGTGCCATGGTGGAGAACTGGGATGTTACAAAGGTGACTAT 541

QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGATGAGAACCAACATCTCCATTACAAAT 420

DB 542 TATAAGGATGGTGAAGCTCTCAAGTACTGATGAGAACCAACATCTCCATTACAAAT 601

QY 421 GCCACAGTTGAAGCAGTGGAACTTACTGTTACGGGCAAGTGGGAGTGGACTAT 480

DB 602 GCCACAGTTGAAGCAGTGGAACTTACTGTTACGGGCAAGTGGGAGTGGACTAT 661

QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516

DB 662 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 697

Search completed: October 8, 2004, 23:17:40

Job time : 251.898 secs

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Sequence 15, Appl  
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44 279.2 54.1 522 3 US-09-005-299-14  
45 279.2 54.1 522 3 US-09-005-299-15

ALIGNMENTS

RESULT 1  
US-08-756-387B-12  
; Sequence 12, Application US/08756387B  
; Patent No. 5945294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect IgE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESS: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,387B  
FILING DATE: No. 5945294ember 26, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 516 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..516  
US-08-756-387B-12

Query Match 100.0%; Score 516; DB 2; Length 516;  
Best Local Similarity 100.0%; Pred. No. 6.5e-16;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

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Searched: 682709 seqs, 277475446 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	516	100.0	516	4	US-09-285-873-12
3	516	100.0	516	4	US-09-944-277A-12
4	516	100.0	591	2	US-08-756-387B-10
5	516	100.0	591	4	US-09-285-873-10
6	516	100.0	591	4	US-09-944-277A-10
7	516	100.0	699	2	US-08-756-387B-7
8	516	100.0	699	4	US-09-285-873-7
9	516	100.0	699	4	US-09-944-277A-7
10	516	100.0	713	2	US-08-238-027-3
11	516	100.0	773	4	US-08-897-956A-6
12	516	100.0	774	2	US-08-756-387B-4
13	516	100.0	774	2	US-08-756-387B-5
14	516	100.0	774	4	US-09-285-873-4
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24	516	100.0	1198	4	US-09-944-277A-1
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QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTATAAGGAGAG 60  
Db 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTATAAGGAGAG 60  
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120  
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120  
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Db 121 CACATGCGAGCTTTTCAAGAGAGACAATTCAGGTTTGAATATGTAATGCCAAATTT 180  
QY 181 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db 181 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
QY 241 CTGGAAGTCTTCAAGTCTGCTCTTCAAGGCTCTGCTGAGGCTGCTGAGGCTGAGGAGGC 300  
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QY 301 CAGCCCTCTTCTCAGTGGCCATGCTGAGGAACTGGGATGTTACAAAGGTGATCTAT 360  
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QY 361 TATAAGTGTGAGCTCTCAAGTCTGCTGAGTGTGAGAACCAACATCTCCATTACAAAT 420  
Db 361 TATAAGTGTGAGCTCTCAAGTCTGCTGAGTGTGAGAACCAACATCTCCATTACAAAT 420  
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTCAGGGCAAGTGTGGAGCTGAGTAT 480  
Db 421 GCCACAGTTGAAGACAGTGGAACTTACTGTCAGGGCAAGTGTGGAGCTGAGTAT 480  
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516  
Db 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

## RESULT 2

US-09-285-873-12  
; Sequence 12, Application US/09285873  
; Patent No. 6309832  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/285,873  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/756,387  
; FILING DATE: No. 6309832ember 26, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 516 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..516  
; US-09-285-873-12  
  
Query Match 100.0%; Score 516; DB 4; Length 516;  
Best Local Similarity 100.0%; Pred. No. 6.5e-161;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTATAAGGAGAG 60  
Db 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCTCCATGGAATAGAATATTATAAGGAGAG 60  
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120  
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120  
QY 121 CACATGCGAGCTTTTCAAGAGAGACAATTCAGGTTTGAATATGTAATGCCAAATTT 180  
Db 121 CACATGCGAGCTTTTCAAGAGAGACAATTCAGGTTTGAATATGTAATGCCAAATTT 180  
QY 181 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db 181 GAAGACAGTGGAGATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
QY 241 CTGGAAGTCTTCAAGTCTGCTCTTCAAGGCTCTGCTGAGGCTGCTGAGGCTGAGGAGGC 300  
Db 241 CTGGAAGTCTTCAAGTCTGCTCTTCAAGGCTCTGCTGAGGCTGCTGAGGCTGAGGAGGC 300  
QY 301 CAGCCCTCTTCTCAGTGGCCATGCTGAGGAACTGGGATGTTACAAAGGTGATCTAT 360  
Db 301 CAGCCCTCTTCTCAGTGGCCATGCTGAGGAACTGGGATGTTACAAAGGTGATCTAT 360  
QY 361 TATAAGTGTGAGCTCTCAAGTCTGCTGAGTGTGAGAACCAACATCTCCATTACAAAT 420  
Db 361 TATAAGTGTGAGCTCTCAAGTCTGCTGAGTGTGAGAACCAACATCTCCATTACAAAT 420  
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTCAGGGCAAGTGTGGAGCTGAGTAT 480  
Db 421 GCCACAGTTGAAGACAGTGGAACTTACTGTCAGGGCAAGTGTGGAGCTGAGTAT 480  
QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516  
Db 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

## RESULT 3

US-09-944-277A-12  
; Sequence 12, Application US/09944277A  
; Patent No. 6682894  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado

COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Wordperfect for Windows, Version 7.0  
CURRENT APPLICATION DATA: US/09/944,277A  
APPLICATION NUMBER: US/09/944,277A  
FILING DATE: 30-AUG-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/285,873  
FILING DATE: 1999-03-31  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 516 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..516  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-09-944-277A-12  
  
Query Match 100.0%; Score 516; DB 4; Length 516;  
Best Local Similarity 100.0%; Pred. No. 6.5e-161; Indels 0; Gaps 0;  
Matches 516; Conservative 0; Mismatches 0;  
  
Qy 1 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAG 60  
Db 1 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAG 60  
  
Qy 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120  
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAATGGTTC 120  
  
Qy 121 CACAAATGCGAGCCTTTCCAGAGAGACAATTTCAAGTTTGAATTTGTGAATGCCAAATTT 180  
Db 121 CACAAATGCGAGCCTTTCCAGAGAGACAATTTCAAGTTTGAATTTGTGAATGCCAAATTT 180  
  
Qy 181 GAAGACAGTGGAGAAATACAAATGTGAGACCAACCAAGTGAATGAGAGTGAACCTGTGTAC 240  
Db 181 GAAGACAGTGGAGAAATACAAATGTGAGACCAACCAAGTGAATGAGAGTGAACCTGTGTAC 240  
  
Qy 241 CTGGAAGTCTTCAAGTGTGCTCTCTTCCAGGCTCTGCTGAGGTTGATGGAGGC 300  
Db 241 CTGGAAGTCTTCAAGTGTGCTCTCTTCCAGGCTCTGCTGAGGTTGATGGAGGC 300  
  
Qy 301 CAGCCCTCTTCCCTCAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 360  
Db 301 CAGCCCTCTTCCCTCAGTGGCCATGGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 360  
  
Qy 361 TATAAGATGTGAGCTCTCAAGTGTGCTGATGAGACCAACACATCTCCATTACAAAT 420  
Db 361 TATAAGATGTGAGCTCTCAAGTGTGCTGATGAGACCAACACATCTCCATTACAAAT 420  
  
Qy 421 GCCACAGTTGAAGCAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGAATAT 480  
Db 421 GCCACAGTTGAAGCAGTGGAACTTACTGTACGGGCAAGTGTGGCAGCTGGAATAT 480  
  
Qy 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516  
Db 481 GAGTCTGAGCCCTCAACATTACTGTATAAAGCT 516

RESULT 4  
US-08-756-387B-10  
Sequence 10, Application US/08756387B  
Patent No. 5945294  
GENERAL INFORMATION:  
APPLICANT: Frank, Glenn R.  
APPLICANT: Porter, James P.  
APPLICANT: Rushlow, Keith E.  
APPLICANT: Wassom, Donald L.  
TITLE OF INVENTION: Method to Detect Ige  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
ADDRESS: Heska Corporation  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Wordperfect for Windows, Version 7.0  
CURRENT APPLICATION DATA: US/08/756,387B  
APPLICATION NUMBER: US/08/756,387B  
FILING DATE: No. 5945294ember 26, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 591 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..591  
US-08-756-387B-10  
  
Query Match 100.0%; Score 516; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 7.1e-161;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAG 60  
Db 76 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAG 135  
  
Qy 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120  
Db 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 195  
  
Qy 121 CACAATGGCAGCCTTTCCAGAGAGACAATTTCAAGTTTGAATTTGTGAATGCCAAATTT 180  
Db 196 CACAATGGCAGCCTTTCCAGAGAGACAATTTCAAGTTTGAATTTGTGAATGCCAAATTT 255  
  
Qy 181 GAAGACAGTGGAGAAATACAAATGTGAGACCAACCAAGTGAATGAGAGTGAACCTGTGTAC 240  
Db 256 GAAGACAGTGGAGAAATACAAATGTGAGACCAACCAAGTGAATGAGAGTGAACCTGTGTAC 315  
  
Qy 241 CTGGAAGTCTTCAAGTGTGCTCTCTTCCAGGCTCTGCTGAGGTTGATGGAGGC 300  
Db 316 CTGGAAGTCTTCAAGTGTGCTCTCTTCCAGGCTCTGCTGAGGTTGATGGAGGC 375

QY 301 CAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTTGTAACAAGTGATCTAT 360  
 Db 376 CAGCCCTCTTCTCAGGTGCCATGGTTGGAGAACTGGGATGTTGTAACAAGTGATCTAT 435  
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACACATCTCCATTACAAAT 420  
 Db 436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACACATCTCCATTACAAAT 495  
 QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTAGCGGCAAGTGTGCGAGCTGGACTAT 480  
 Db 496 GCCACAGTTGAAGACAGTGGAACTTACTGTAGCGGCAAGTGTGCGAGCTGGACTAT 555  
 QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAAGCT 516  
 Db 556 GAGTCTGAGCCCTCAACATTACTGTAATAAAAGCT 591

## RESULT 5

US-09-285-873-10  
 ; Sequence 10, Application US/09285873  
 ; Patent No. 6309832

## GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.  
 APPLICANT: Porter, James P.  
 APPLICANT: Rushlow, Keith E.  
 APPLICANT: Wassom, Donald L.

TITLE OF INVENTION: Method to Detect Ige

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/285,873

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/756,387

FILING DATE: No. 6309832ember 26, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 591 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..591

US-09-285-873-10

Query Match 100.0%; Score 516; DB 4; Length 591;

Best Local Similarity 100.0%; Pred. No. 7.1e-161;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 60

Db 76 GTCCCTCAGAAACCTAAGGTCTCTTGAACCCCTCCATGGAATAGAAATATTTAAAGGAGAG 135  
 QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGTTCCACCAAAATGGTTTC 120  
 Db 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGTTCCACCAAAATGGTTTC 195  
 QY 121 CACAATGGGAGCCTTTCAAGAAGAGACAAATTTCAAGTTTGAATATTGTGAATGCCAAATTT 180  
 Db 196 CACAATGGGAGCCTTTCAAGAAGAGACAAATTTCAAGTTTGAATATTGTGAATGCCAAATTT 255  
 QY 181 GAAGACAGTGGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
 Db 256 GAAGACAGTGGGAGAAATACAAATGTGAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 315  
 QY 241 CTGGAAGTCTTCAAGTACTGGCTGTCTTCAAGGCTCTGTGAGGTGGTGTAGAGGGC 300  
 Db 316 CTGGAAGTCTTCAAGTACTGGCTGTCTTCAAGGCTCTGTGAGGTGGTGTAGAGGGC 375  
 QY 301 CAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTTGTAACAAGTGATCTAT 360  
 Db 376 CAGCCCTCTTCTCAGGTGCCATGGTTGGAGGAACTGGGATGTTGTAACAAGTGATCTAT 435  
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACACATCTCCATTACAAAT 420  
 Db 436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACACATCTCCATTACAAAT 495  
 QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTAGCGGCAAGTGTGCGAGCTGGACTAT 480  
 Db 496 GCCACAGTTGAAGACAGTGGAACTTACTGTAGCGGCAAGTGTGCGAGCTGGACTAT 555  
 QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAAGCT 516  
 Db 556 GAGTCTGAGCCCTCAACATTACTGTAATAAAAGCT 591

## RESULT 6

US-09-944-277A-10  
 ; Sequence 10, Application US/09944277A  
 ; Patent No. 6682894

## GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.  
 Porter, James P.  
 Rushlow, Keith E.  
 Wassom, Donald L.

TITLE OF INVENTION: Method to Detect Ige

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/944,277A

FILING DATE: 30-Aug-2001

CLASSIFICATION: <UNKNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873

FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,387B  
FILING DATE: No. 5945294ember 26, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 699 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..699  
US-08-756-387B-7

Query Match 100.0%; Score 516; DB 2; Length 699;  
Best Local Similarity 100.0%; Pred. No. 7.9e-161;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 60  
DB 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 60  
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120  
DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120  
QY 121 CACAATGGCAGCCTTTCAAGAGACAAATTCAGTTTGAATATTTGAATGCCAAATTT 180  
DB 121 CACAATGGCAGCCTTTCAAGAGACAAATTCAGTTTGAATATTTGAATGCCAAATTT 180  
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTAAATGAGAGTGAACCTGTGTAC 240  
DB 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTAAATGAGAGTGAACCTGTGTAC 240  
QY 241 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGGCTCTCTGAGGCTCTGATGGAGGC 300  
DB 241 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGGCTCTCTGAGGCTCTGATGGAGGC 300  
QY 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGATGTGTACAAAGTGTCTAT 360  
DB 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACCTGGATGTGTACAAAGTGTCTAT 360  
QY 361 TATAAGGATGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 420  
DB 361 TATAAGGATGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACATCTCCATTAACAAT 420  
QY 421 GCCACAGTGAAGACAGTGGAACTTACTACTGTACGGCAAGTGTGGCAGCTGGACTAT 480  
DB 421 GCCACAGTGAAGACAGTGGAACTTACTACTGTACGGCAAGTGTGGCAGCTGGACTAT 480  
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516  
DB 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516

RESULT 8  
US-09-285-873-7  
; Sequence 7, Application US/09285873  
; Patent No. 6309832

INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 591 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..591  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-09-944-277A-10

Query Match 100.0%; Score 516; DB 4; Length 591;  
Best Local Similarity 100.0%; Pred. No. 7.1e-161;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 60  
DB 76 GTCCCTCAGAAACCTTAAGTCTCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 135  
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAAGTTCACCAATGGTTC 120  
DB 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAAGTTCACCAATGGTTC 195  
QY 121 CACAATGGCAGCCTTTCAAGAGACAAATTCAGTTTGAATATTTGAATGCCAAATTT 180  
DB 196 CACAATGGCAGCCTTTCAAGAGACAAATTCAGTTTGAATATTTGAATGCCAAATTT 255  
QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTAAATGAGAGTGAACCTGTGTAC 240  
DB 256 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAAGTAAATGAGAGTGAACCTGTGTAC 315  
QY 241 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGGCTCTCTGAGTGGTGTGAGGAGGC 300  
DB 316 CTGGAAGTCTTCAAGTGAAGTGGTCTCTTCAAGGCTCTCTGAGTGGTGTGAGGAGGC 375  
QY 301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGAACTGGATGTGTACAAAGTGTCTAT 360  
DB 376 CAGCCCTCTTCTCAGTGGCCATGTTGGAGAACTGGATGTGTACAAAGTGTCTAT 435  
QY 361 TATAAGGATGTGAAGCTCTCAAGTACTGTATGAGAACCAACATCTCCATTAACAAT 420  
DB 436 TATAAGGATGTGAAGCTCTCAAGTACTGTATGAGAACCAACATCTCCATTAACAAT 495  
QY 421 GCCACAGTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480  
DB 496 GCCACAGTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 555  
QY 481 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 516  
DB 556 GAGTCTGAGCCCTCAACATTTACTGTATAAAGCT 591

RESULT 7  
US-08-756-387B-7  
; Sequence 7, Application US/08756387B  
; Patent No. 5945294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESS: Heskia Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525



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/ APPLICATION NUMBER: JP 4-270515
/ FILING DATE: 08-OCT-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 5-208217
/ FILING DATE: 29-JUL-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 5-197341
/ FILING DATE: 09-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 5-251605
/ FILING DATE: 07-OCT-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 5-251606
/ FILING DATE: 07-OCT-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 5-251608
/ FILING DATE: 07-OCT-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 5-261355
/ FILING DATE: 19-OCT-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 5-264802
/ FILING DATE: 22-OCT-1993
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-293-7060
/ TELEFAX: 202-293-7860
/ TELEX: 6491103
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 713 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 120..713
/ IDENTIFICATION METHOD: by similarity with known
/ IDENTIFICATION METHOD: sequence or to an established consensus
/
US-08-238-027-3

Query Match          100.0%; Score 516; DB 2; Length 713;
Best Local Similarity 100.0%; Pred. No. 8e-161;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1   GTCCTCAGAAACCTAAGGTCCTCCTTGAACCCCTCCATGGAATAGAATATTTAAAGGAGAG 60
DB      195  GTCCCTCAGAAACCTAAGGTCCTCTTGAAACCCCTCAATGGAATAGAATATTTAAAGGAGAG 254

QY      61   AATGTGACTCTTACATGAATATGGGAACAATTTCTTTGAAGTCAGTCTCCACCAATATGGTTC 120
DB      255  AATGTGACTCTTACATGAATATGGGAACAATTTCTTTGAAGTCAGTCTCCACCAATATGGTTC 314

QY      121  CACAATGGCAGCCCTTTCAGAAAGACACAAATTCAGATTTTGAATATTTGTAATGCCAAATTT 180
DB      315  CACAATGGCAGCCCTTTCAGAAAGACACAAATTCAGATTTTGAATATTTGTAATGCCAAATTT 374

QY      181  GAAGACAGTGGAGAATACAAATGTCACACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240
DB      375  GAAGACAGTGGAGAATACAAATGTCACACCAACAAGTTAATGAGAGTGAACCTGTGTAC 434

QY      241  CTGGAAGCTCTTCAGTGACTGGCTCTCCTTTCAGGCCCTCTGCTGAGGTGGTGTGATGGAGGC 300
DB      435  CTGGAAGCTCTTCAGTGACTGGCTCTCCTTTCAGGCCCTCTGCTGAGGTGGTGTGATGGAGGC 494

QY      301  CAGCCCTCTTCTTCAGGTGCCATGTTGGAGGAACCTGGGATGTGTACAAGTGATCTAT 360
DB      495  CAGCCCTCTTCTTCAGGTGCCATGTTGGAGGAACCTGGGATGTGTACAAGTGATCTAT 554

QY      361  TATAAGATGGTGAAGCTCTCAAGTACTGGTATGAGBACCACACATCTCCATTACAAT 420

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Db			
121	QY	CACAATGGCAGCCCTTTGAGAGAGACAAATTCAGTTTGAATATGTGAAATGCGCAAAATTT	180
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121	QY	CACAATGGCAGCCCTTTGAGAGAGACAAATTCAGTTTGAATATGTGAAATGCGCAAAATTT	180
Db			
181	QY	GAAGACAGTGAGAGAAATCAAAATGTCAGCACCAACAAAGTTAAATGAGAGTGAACCTGTGTAC	240
Db			
181	QY	GAAGACAGTGAGAGAAATCAAAATGTCAGCACCAACAAAGTTAAATGAGAGTGAACCTGTGTAC	240
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241	QY	CTGGAAGTCCTTCAGTGACTGGCTGCTCCCTTCAGGCCCTCTGCTGAGTGTGATGAGGGC	300
Db			
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301	QY	CAGCCCTCTTCCTCAGTGCCATGGTTGGAGAACTGGGATCTGTACAAGTGTATCTAT	360
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361	QY	TATAAGGATGTTGAAGTCTTCAAGTACTCGTATGAGAACCAACAATCTCCATTTACAAT	420
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; Sequence 3, Application US/08238027			
; Patent No. 5874404			
; GENERAL INFORMATION:			
; APPLICANT: RA. CHISEI			
; APPLICANT: NAITO, KOJI			
; APPLICANT: HIRAMA, MINORU			
; APPLICANT: OKUMURA, KO			
; TITLE OF INVENTION: ANTIALLERGIC COMPOSITION			
; NUMBER OF SEQUENCES: 3			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS			
; STREET: 2100 PENNSYLVANIA AVENUE			
; CITY: N.W.			
; STATE: WASHINGTON, D.C.			
; COUNTRY: U.S.A.			
; ZIP: 20037-3202			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/238,027			
; FILING DATE: 03-MAY-1994			
; CLASSIFICATION: 800			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: JP 4-229227			
; FILING DATE: 04-AUG-1992			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: JP 4-213002			
; FILING DATE: 10-AUG-1992			
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; APPLICATION NUMBER: JP 4-270513			
; FILING DATE: 08-OCT-1992			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: JP 4-270514			
; FILING DATE: 08-OCT-1992			
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; Sequence 6, Application US/08897956A  
; Patent No. 6423512  
; GENERAL INFORMATION:  
; APPLICANT: Mary Ellen Digan  
; APPLICANT: Philip Lake  
; APPLICANT: Hermann Gram  
; TITLE OF INVENTION: Fusion Polypeptides  
; FILE REFERENCE: 600-7244/CPA  
; CURRENT APPLICATION NUMBER: US/08/897,956A  
; CURRENT FILING DATE: 1997-07-21  
; PRIOR APPLICATION NUMBER: 60/022,689  
; PRIOR FILING DATE: 1996-07-26  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 773  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fusion Polynucleotide  
US-08-897-956A-6

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Best Local Similarity 100.0%; Pred. No. 8.4e-161;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 CACAATGGCAGCCCTTTCAGAGAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 180  
Db 196 CACAATGGCAGCCCTTTCAGAGAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 255  
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Db 316 CTGGAAGTCTTCAAGTCAAGTGGCTCTCTTCAAGCCCTCTGCTGAGTGGTGTGAGGGC 375

Qy 301 CAGCCCTCTTCTCAGGTGCCATGTTGGAGAACTGGATGTGTACAAAGTGAATCTAT 360  
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Qy 361 TATAAGATGGTCAAGCTCTCAAGTACTGTATGAGAAACCAACAATCTCCATTACAAT 420  
Db 436 TATAAGATGGTCAAGCTCTCAAGTACTGTATGAGAAACCAACAATCTCCATTACAAT 495  
Qy 421 GCACAGTTGAAGACAGTGGAACTACTACTGTACGGGAAAGTGGGAGCTGGACTAT 480  
Db 496 GCACAGTTGAAGACAGTGGAACTACTACTGTACGGGAAAGTGGGAGCTGGACTAT 555  
Qy 481 GAGTCTGAGCCCTCAACATCTACTGTATATAAAGCT 516

Db 556 GAGTCTGAGCCCTCAACATCTACTGTATATAAAGCT 591

RESULT 12  
US-08-756-387B-4  
; Sequence 4, Application US/08756387B  
; Patent No. 5945294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wasson, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387B  
; FILING DATE: No. 5945294ember 26, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 774 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..774  
US-08-756-387B-4

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Best Local Similarity 100.0%; Pred. No. 8.4e-161;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 256 GAGACAGTGGAGAAATCAAAATGTGAGCAACCAACAATTAATGAGAGTGAACCTGTGTAC 315  
Qy 241 CTGGAAGTCTTCAAGTCAAGTGGCTCTCTTCAAGCCCTCTGCTGAGTGGTGTGAGGGC 300  
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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774
US-09-285-873-4

Query Match      100.0%; Score 516; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 8.4e-161;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAACCTTAAGGCTCTCTGAAACCCCTCCATGGAATAGATATTTAAAGGAGG 60
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QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120
Db 136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 195
QY 121 CACATGGCCCTTTTCAGAGAGACAAATTCAGTTTGAATTTGTGAATGCCAAATTT 180
Db 196 CACATGGCCCTTTTCAGAGAGACAAATTCAGTTTGAATTTGTGAATGCCAAATTT 255
QY 181 GAAGACAGTGGAGAAATACAAATGTGACACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240
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QY 301 CAGCCCTCTTCTCAGTCCCATGTTGGAGAACTGGGATGTGTACAAAGTGTATCTAT 360
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QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAAAT 420
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QY 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516
Db 556 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 591

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## RESULT 15

US-09-285-873-5/c  
 ; Sequence 5, Application US/09285873  
 ; Patent No. 6309832

## GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.  
 ; APPLICANT: Porter, James P.  
 ; APPLICANT: Rushlow, Keith E.  
 ; APPLICANT: Wassom, Donald L.  
 ; TITLE OF INVENTION: Method to Detect IgE  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.  
 ; ADDRESSEE: Heska Corporation  
 ; STREET: 1825 Sharp Point Drive  
 ; CITY: Fort Collins  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80525  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: WordPerfect for Windows, Version 7.0  
 ; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/285.873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756.387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-285-873-5

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Query Match 100.0%; Score 516; DB 4; Length 774;

Best Local Similarity 100.0%; Pred. No. 8.4e-161;

Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ALIGNMENTS

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; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wasson, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/944,277A  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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3	516	100.0	528	10	US-09-809-715-1
4	516	100.0	528	13	US-10-293-992-1
5	516	100.0	591	9	US-09-944-277A-10
6	516	100.0	699	9	US-09-944-277A-7
7	516	100.0	774	9	US-09-944-277A-4
8	516	100.0	774	9	US-09-944-277A-5
9	516	100.0	898	13	US-10-236-392-27
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11	516	100.0	1198	9	US-09-944-277A-3
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;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..516
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Best Local Similarity 100.0%; Pred. No. 2e-157;
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QY 1 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCATGGAATAGAAATTTAAAGGAGAG 60
DB 1 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCATGGAATAGAAATTTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCGCAAAATTT 180
DB 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCGCAAAATTT 180
QY 181 GAACACAGTGGAGATACAAATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 181 GAACACAGTGGAGATACAAATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
QY 241 CTGGAAGTCTTTCAGTACTGGCTGCTCTTTCAGGCGCTCTCTCTGAGGTGGTGGAGGGG 300
DB 241 CTGGAAGTCTTTCAGTACTGGCTGCTCTTTCAGGCGCTCTCTCTGAGGTGGTGGAGGGG 300
QY 301 CAGCCCTCTTCTCAGTGCCTCATGTTGAGGAACTGGGATGTGTACAGGTGATCTAT 360
DB 301 CAGCCCTCTTCTCAGTGCCTCATGTTGAGGAACTGGGATGTGTACAGGTGATCTAT 360
QY 361 TATAAGATGGTGAAGTCTCAAGTACTGTGATGAGAACCAACAATCTCCATTACAAAT 420
DB 361 TATAAGATGGTGAAGTCTCAAGTACTGTGATGAGAACCAACAATCTCCATTACAAAT 420
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGGCAGCTGGACTAT 480
DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGGCAGCTGGACTAT 480
QY 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516
DB 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516

RESULT 2
US-10-293-992-3
; Sequence 3, Application US/10293992
; Publication No. US2004003327A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR
; FILE REFERENCE: AL-3-Cl-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 1999-11-04
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 6
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(516)
;   OTHER INFORMATION:
US-10-293-992-3

Query Match      100.0%; Score 516; DB 13; Length 516;
Best Local Similarity 100.0%; Pred. No. 2e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCATGGAATAGAAATTTAAAGGAGAG 60
DB 1 GTCCTCAGAAACCTAAGGTCCTCTTGAACCCCTCATGGAATAGAAATTTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
DB 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120
QY 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCGCAAAATTT 180
DB 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGTTTGAATTTGAATGCGCAAAATTT 180
QY 181 GAACACAGTGGAGATACAAATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
DB 181 GAACACAGTGGAGATACAAATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240
QY 241 CTGGAAGTCTTTCAGTACTGGCTGCTCTTTCAGGCGCTCTCTCTGAGGTGGTGGAGGGG 300
DB 241 CTGGAAGTCTTTCAGTACTGGCTGCTCTTTCAGGCGCTCTCTCTGAGGTGGTGGAGGGG 300
QY 301 CAGCCCTCTTCTCAGTGCCTCATGTTGAGGAACTGGGATGTGTACAGGTGATCTAT 360
DB 301 CAGCCCTCTTCTCAGTGCCTCATGTTGAGGAACTGGGATGTGTACAGGTGATCTAT 360
QY 361 TATAAGATGGTGAAGTCTCAAGTACTGTGATGAGAACCAACAATCTCCATTACAAAT 420
DB 361 TATAAGATGGTGAAGTCTCAAGTACTGTGATGAGAACCAACAATCTCCATTACAAAT 420
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGGCAGCTGGACTAT 480
DB 421 GCCACAGTTGAAGACAGTGGAACTTACTGTACGGGCAAAAGTGGCAGCTGGACTAT 480
QY 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516
DB 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516

RESULT 3
US-09-809-715-1
; Sequence 1, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC EPSILON RECEPTOR AND AN ANTIBODY
; FILE REFERENCE: AL-8
; CURRENT APPLICATION NUMBER: US/09/809,715
; CURRENT FILING DATE: 2001-03-14
; PRIOR FILING DATE: 1999-03-15
; PRIOR FILING DATE: 1998-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 528
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(528)
US-09-809-715-1

Query Match      100.0%; Score 516; DB 10; Length 528;
Best Local Similarity 100.0%; Pred. No. 2e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCCTCAGAAACCTAAGTCTCCTTGAACCCCTCATGGATAGAAATTTAAAGGAGAG 60
Db 1 GTCCCTCAGAAACCTAAGTCTCCTTGAACCCCTCATGGATAGAAATTTAAAGGAGAG 60
Qy 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 120
Db 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 120
Qy 121 CACAATGGCAGCCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATTTGAATGCGCAATTT 180
Db 121 CACAATGGCAGCCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATTTGAATGCGCAATTT 180
Qy 181 GAAGACAGTGGAGATACAAATGTCAGCAGCAGCAACAGTTAATGAGAGTGAACCTGTGTAC 240
Db 181 GAAGACAGTGGAGATACAAATGTCAGCAGCAGCAACAGTTAATGAGAGTGAACCTGTGTAC 240
Qy 241 CTGGAAGTCTTCAAGTGGTGGTCTTCTCCTTCAAGGCTCTCTCTGAGTGGTGAAGGGC 300
Db 241 CTGGAAGTCTTCAAGTGGTGGTCTTCTCCTTCAAGGCTCTCTCTGAGTGGTGAAGGGC 300
Qy 301 CAGCCCTCTTCTCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
Db 301 CAGCCCTCTTCTCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
Qy 361 TATAAGGATGGTGAAGTCTTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
Db 361 TATAAGGATGGTGAAGTCTTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
Qy 421 GCCACAGTTGAAGACAGTGGAACTTACTTACTGTAACGGGCAAAAGTGGCAGCTGGACTAT 480
Db 421 GCCACAGTTGAAGACAGTGGAACTTACTTACTGTAACGGGCAAAAGTGGCAGCTGGACTAT 480
Qy 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516
Db 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516
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RESULT 5

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US-09-944-277A-10
; Sequence 10, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(528)
US-09-809-715-1

Query Match      100.0%; Score 516; DB 10; Length 528;
Best Local Similarity 100.0%; Pred. No. 2e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCCCTCAGAAACCTAAGTCTCCTTGAACCCCTCATGGATAGAAATTTAAAGGAGAG 60
Db 1 GTCCCTCAGAAACCTAAGTCTCCTTGAACCCCTCATGGATAGAAATTTAAAGGAGAG 60
Qy 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 120
Db 61 AATGTGACTCTTACATGTAATGGGACAAATTTCTTTGAAGTCAGTTCACCAAAATGTTTC 120
Qy 121 CACAATGGCAGCCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATTTGAATGCGCAATTT 180
Db 121 CACAATGGCAGCCCTTTTCAAGAGAGACAAATTTCAAGTTTGAATTTGAATGCGCAATTT 180
Qy 181 GAAGACAGTGGAGATACAAATGTCAGCAGCAGCAACAGTTAATGAGAGTGAACCTGTGTAC 240
Db 181 GAAGACAGTGGAGATACAAATGTCAGCAGCAGCAACAGTTAATGAGAGTGAACCTGTGTAC 240
Qy 241 CTGGAAGTCTTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
Db 241 CTGGAAGTCTTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
Qy 301 CAGCCCTCTTCTCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
Db 301 CAGCCCTCTTCTCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
Qy 361 TATAAGGATGGTGAAGTCTTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
Db 361 TATAAGGATGGTGAAGTCTTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
Qy 421 GCCACAGTTGAAGACAGTGGAACTTACTTACTGTAACGGGCAAAAGTGGCAGCTGGACTAT 480
Db 421 GCCACAGTTGAAGACAGTGGAACTTACTTACTGTAACGGGCAAAAGTGGCAGCTGGACTAT 480
Qy 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516
Db 481 GAGTCTGAGCCCTCAACATTACTGTAATAAAGCT 516
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RESULT 4

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US-10-293-992-1
; Sequence 1, Application US/10293992
; Publication No. US2004003527A1
; GENERAL INFORMATION:
; APPLICANT: Jardtetzky, Theodore S.
; Garman, Scott Clayton
; Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR
; FILE REFERENCE: AL-3-C1-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/434,193
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,219
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
;
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..591
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-944-277A-10

Query Match 100.0%; Score 516; DB 9; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.1e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTAAGGCTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 60
DB 76 GTCCCTCAGAACCTAAGGCTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 135
QY 61 AATGTGACTCTTACATGTATGGAACAAATTTCTTGAAGTCAGTTCCACCAATGTTTC 120
DB 136 AATGTGACTCTTACATGTATGGAACAAATTTCTTGAAGTCAGTTCCACCAATGTTTC 195
QY 121 CACAATGGCAGCCTTTTCAAGAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 180
DB 196 CACAATGGCAGCCTTTTCAAGAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 255
QY 181 GAACACAGTGGAGAAATACAAATGTCAGCACCAACAAAGTAAATGAGAGTGAACCTGTAC 240
DB 256 GAACACAGTGGAGAAATACAAATGTCAGCACCAACAAAGTAAATGAGAGTGAACCTGTAC 315
QY 241 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 360
DB 316 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 375
QY 301 CAGCCCTCTTCTCAGTGCCTGCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 360
DB 376 CAGCCCTCTTCTCAGTGCCTGCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 435
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
DB 436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 495
QY 421 GCCACAGTTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGCAGTGGACTAT 480
DB 496 GCCACAGTTGAAGACAGTGAACCTACTACTGTACGGGCAAGTGTGGCAGTGGACTAT 555
QY 481 GAGTCTGAGCCCTTCAACATTACTGTAAATAAAGCT 516
DB 556 GAGTCTGAGCCCTTCAACATTACTGTAAATAAAGCT 591

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## RESULT 6

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US-09-944-277A-7
; Sequence 7, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.

```

```

;
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Carol Talkington Verser, Ph.D.
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk.
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
;
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 699 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..699
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-944-277A-7

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Query Match 100.0%; Score 516; DB 9; Length 699;
Best Local Similarity 100.0%; Pred. No. 2.4e-157;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTAAGGCTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 60
DB 1 GTCCCTCAGAACCTAAGGCTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 60
QY 61 AATGTGACTCTTACATGTATGGAACAAATTTCTTGAAGTCAGTTCCACCAATGTTTC 120
DB 61 AATGTGACTCTTACATGTATGGAACAAATTTCTTGAAGTCAGTTCCACCAATGTTTC 120
QY 121 CACAATGGCAGCCTTTTCAAGAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 180
DB 121 CACAATGGCAGCCTTTTCAAGAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 180
QY 181 GAACACAGTGGAGAAATACAAATGTCAGCACCAACAAAGTAAATGAGAGTGAACCTGTAC 240
DB 181 GAACACAGTGGAGAAATACAAATGTCAGCACCAACAAAGTAAATGAGAGTGAACCTGTAC 240
QY 241 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 360
DB 241 CTGGAAGTCTTCAAGTACTGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 300
QY 301 CAGCCCTCTTCTCAGTGCCTGCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 360
DB 301 CAGCCCTCTTCTCAGTGCCTGCTCTTCAAGGCTCTCTTCAAGGCTCTCTTCAAGGCTCTAT 360
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
DB 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420

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	Qy	121	CACAAATGGGAGCCCTTTTCAGAGAAGACAAAATTCAAGTTTGAATAATTGTGAATGCCAATAATTT	180
	Dd	196	CACAAATGGGAGCCCTTTTCAGAAGAGACAAAATTCAGTTTGAATAATTGTGAATGCCAATAATTT	255
	Qy	181	GANGACAGTGGGAATACAAAAATGTCAGACCAACAAGTTAAATCAGAGCTGAAACCTGTGTAC	240
	Dd	256	GAAGACAGTGGGAATACAAAATGTCAGCACCAACAGTTAAATGAGAGTGAAACCTGTGTAC	315
	Qy	241	CTGGAAGTCTTCAGTAGACTGSGCTGCTCCTTCAGGCCTCTCGTCAGGTGGTGATGGAGGGC	300
	Dd	316	CTGGAAGTCTTCAGTGACTGSGCTGCTCCTTCAGGCCTCTCGTCAGGTGGTGATGGAGGGC	375
	Qy	301	CAGCCCCCTTCTCCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAAGGTGATCTAT	360
	Dd	376	CAGCCCCCTTCTCCTCAGGTGCCATGGTTGGAGGAACCTGGGATGTGTACAAAGGTGATCTAT	435
	Qy	361	TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAAT	420
	Dd	436	TATAAGGATGGTGAAGCTCTCAAGTACTGTGTATGAGAACCAACAATCTCCATTACAAAT	495
	Qy	421	GCCACAGTTGAAGACAGTGGAACTACTTA CTGTACGGGCAAAGTGTGGCAGCTGGACTAT	480
	Dd	496	GCCACAGTTGAAGACAGTGGAACTACTTA CTGTACGGGCAAAGTGTGGCAGCTGGACTAT	555
	Qy	481	GAGTCTGAGCCCCCTCAACATTACTGTGAATAAAGCT	516
	Dd	556	GAGTCTGAGCCCCCTCAACATTACTGTGAATAAAGCT	591

RESULT 8  
US-09-944-277A-5/C  
; Sequence 5, Application US/09944277A  
; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
;

TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 774 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

421	GCACAGTTCAGACAGCTGGAACCTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT	480
421	GCACAGTTCAGACAGCTGGAACCTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT	480
481	GAGTCTGAGCCCCCTCAACATTACTGTAAATAAAGCT	516
481	GAGTCTGAGCCCCCTCAACATTACTGTAAATAAAGCT	516

RESULT 7  
 US-09-944-277A-4  
 ; Sequence 4, Application US/09944277A  
 ; Patent No. US20020034771A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Frank, Glenn R.  
 ; Porter, James P.  
 ; Rushlow, Keith E.  
 ; Wassom, Donald L.  
 ;  
 ; TITLE OF INVENTION: Method to Detect Ige  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.  
 ; Heskia Corporation  
 ; STREET: 1825 Sharp Point Drive  
 ; CITY: Fort Collins  
 ; STATE: Colorado

```

? ZIP: 80525
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: Windows 95
? SOFTWARE: Wordperfect for Windows, Version 7.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: iis/pg/944_277d

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	Query Match	100.0%	Score 516;	DB 9;	Length 774;
	Best Local Similarity	100.0%;	Pred. No. 2.5e-157;		
	Matches 516;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GTCCCTCAGAACCTTAAGGTCCTCTTGAACCCCTCCATGGAAATAGAATATTTAAAGGAGAG	60		
Db	76	GTCCCTCAGAACCTTAAGGTCCTCTTGAACCCCTCCATGGAAATAGAATATTTAAAGGAGAG	135		
Qy	61	AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTTGAAGTCAGTCCACCAAAAGGTTTC	120		
Db	136	AATGTGACTCTTACATGTAATGGGAAACAATTTCTTTTGAAGTCAGTCCACCAAAAGGTTTC	195		

MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-944-277A-5

Query Match  
Best Local Similarity 100.0%; Score 516; DB 9; Length 774;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCTCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 60  
Db  
699 GTCCCTCAGAACCTTAAGTCTCTCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 640

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120  
Db  
639 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 580

QY 121 CACATGAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGGCAATTT 180  
Db  
579 CACATGAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGGCAATTT 520

QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db  
519 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 460

QY 241 CTGGAAGTCTTTCAGTACTGCTCTCTTCCAGCCCTCTGCTGAGGTGGTGTGAGGGC 300  
Db  
459 CTGGAAGTCTTTCAGTACTGCTCTCTTCCAGCCCTCTGCTGAGGTGGTGTGAGGGC 400

QY 301 CAGCCCTCTTCTCAGTGTGCTATGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 360  
Db  
399 CAGCCCTCTTCTCAGTGTGCTATGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 340

QY 361 TATAGAGTGTGAGTCTTCAAGTACTGTTGATGAGAACCAACCAATCTCCATTACAAAT 420  
Db  
339 TATAGAGTGTGAGTCTTCAAGTACTGTTGATGAGAACCAACCAATCTCCATTACAAAT 280

QY 421 GCCACAGTTGAGACAGTGGAACTTACTGTTACGGGCAAGTGTGGCAGCTGGACTAT 480  
Db  
279 GCCACAGTTGAGACAGTGGAACTTACTGTTACGGGCAAGTGTGGCAGCTGGACTAT 220

QY 481 GAGTCTGAGCCCTTCAACATTACTGTATAAAGCT 516  
Db  
219 GAGTCTGAGCCCTTCAACATTACTGTATAAAGCT 184

RESULT 9  
US-10-236-392-27  
Sequence 27, Application US/10236392  
Publication No. US20040067490A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, David W  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Burgess, Catherine, E  
APPLICANT: Casman, Stacie J  
APPLICANT: Catterton, Elina  
APPLICANT: Chapoval, Andrei  
APPLICANT: Crabtree, Julie  
APPLICANT: Edinger, Shlomit, R  
APPLICANT: Ellerman, Karen  
APPLICANT: Gerlach, Valerie  
APPLICANT: Gorman, Linda  
APPLICANT: Grosse, William M  
APPLICANT: Gusev, Vladimir  
APPLICANT: Kekuda, Ramesh  
APPLICANT: LaRoche, William J  
APPLICANT: Li, Li  
APPLICANT: MacDougall, John R  
APPLICANT: Malyankar, Uriel M  
APPLICANT: Miller, Charles E  
APPLICANT: Millet, Isabelle  
APPLICANT: Padigar, Muralidhara  
APPLICANT: Patturajan, Meera  
APPLICANT: Pena, Carol A

APPLICANT: Peyman, John A  
APPLICANT: Pastelli, Luca  
APPLICANT: Reiger, Daniel K  
APPLICANT: Rothenberg, Mark E  
APPLICANT: Shencoy, Suresh  
APPLICANT: Shinkets, Richard A  
APPLICANT: Smithson, Glenda  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 21402-442A  
CURRENT APPLICATION NUMBER: US/10/236,392  
CURRENT FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: US09/540,763  
PRIOR FILING DATE: 2000-03-30  
PRIOR APPLICATION NUMBER: US60/390,155  
PRIOR FILING DATE: 2002-06-19  
PRIOR APPLICATION NUMBER: US09/635,949  
PRIOR FILING DATE: 2000-08-10  
PRIOR APPLICATION NUMBER: US60/318,765  
PRIOR FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: US60/357,303  
PRIOR FILING DATE: 2002-02-15  
PRIOR APPLICATION NUMBER: US60/367,753  
PRIOR FILING DATE: 2002-03-25  
PRIOR APPLICATION NUMBER: US60/369,479  
PRIOR FILING DATE: 2002-04-02  
PRIOR APPLICATION NUMBER: US09/659,634  
PRIOR FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: US60/318,120  
PRIOR FILING DATE: 2001-09-07  
PRIOR APPLICATION NUMBER: US60/318,130  
PRIOR FILING DATE: 2001-09-07  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 794  
SOFTWARE: Custom  
SEQ ID NO 27  
LENGTH: 898  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (26)...(797)  
US-10-236-392-27

Query Match  
Best Local Similarity 100.0%; Score 516; DB 13; Length 898;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCTCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 60  
Db  
101 GTCCCTCAGAACCTTAAGTCTCTCTTGAACCTCCATGGAATAGAAATATTAAAGGAGAG 160

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 120  
Db  
161 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTC 220

QY 121 CACATGAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGGCAATTT 180  
Db  
221 CACATGAGCCCTTTCAGAGAGACAAATTCAGTTTGAATATTGTAATGGCAATTT 280

QY 181 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db  
281 GAAGACAGTGGAGAAATACAAATGTGAGCAACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 340

QY 241 CTGGAAGTCTTTCAGTACTGCTCTCTTCCAGCCCTCTGCTGAGGTGGTGTGAGGGC 300  
Db  
341 CTGGAAGTCTTTCAGTACTGCTCTCTTCCAGCCCTCTGCTGAGGTGGTGTGAGGGC 400

QY 301 CAGCCCTCTTCTCAGTGTGCTATGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 360  
Db  
401 CAGCCCTCTTCTCAGTGTGCTATGTTGGAGGAACCTGGATGTGTACAAGGTGATCTAT 460

QY 361 TATAGAGTGTGAGTCTTCAAGTACTGTTGATGAGAACCAACCAATCTCCATTACAAAT 420

Db 461 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 520  
QY 421 GCCACAGTTGAACAGACAGTGGAACTTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480  
Db 521 GCCACAGTTGAACAGACAGTGGAACTTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 580  
QY 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516  
Db 581 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 616

RESULT 10  
US-09-944-277A-1  
; Sequence 1, Application US/09944277A  
; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect IGE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/944,277A  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 1:  
; NAME/KEY: CDS  
; LOCATION: 107..877  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-944-277A-1

Query Match 100.0%; Score 516; DB 9; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 3.4e-157;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAAACCTTAAGTCTCTCGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 60  
Db 182 GTCCCTCAGAAACCTTAAGTCTCTCGAACCCCTCCATGGAATAGAAATTTAAAGGAGAG 241  
QY 61 AATGTGACTCTTACATGTAATGGGAAATTTCTTTGAAGTCAGTTCCACAAATGGTTC 120  
Db 242 AATGTGACTCTTACATGTAATGGGAAATTTCTTTGAAGTCAGTTCCACAAATGGTTC 301

QY 121 CACAATGCGACGCTTTTCAGAAAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 180  
Db 302 CACAATGCGACGCTTTTCAGAAAGAGACAAATTCAGTTTGAATATTTGTAATGCCAAATTT 361  
QY 181 GAACACAGTGGAGAAATACAAATGTCAGACCAACAGTTTAATGAGAGTGAACCTGTGTAC 240  
Db 362 GAACACAGTGGAGAAATACAAATGTCAGACCAACAGTTTAATGAGAGTGAACCTGTGTAC 421  
QY 241 CTGGAAGTCTTCAAGTGGCTGCTCTTTCAGGCGCTCTCTGAGGTGGTGGAGGGC 300  
Db 422 CTGGAAGTCTTCAAGTGGCTGCTCTTTCAGGCGCTCTCTGAGGTGGTGGAGGGC 481  
QY 301 CAGCCCTCTTCTTCAGTGGTGGAGAACTGGGAACTGGGAACTGGTGTACAAAGGTGATCTAT 360  
Db 482 CAGCCCTCTTCTTCAGTGGTGGAGAACTGGGAACTGGGAACTGGTGTACAAAGGTGATCTAT 541  
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGTGATGAGAACCAACACATCTCCATTACAAAT 420  
Db 542 TATAAGGATGGTGAAGCTCTCAAGTACTGTGATGAGAACCAACACATCTCCATTACAAAT 601  
QY 421 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480  
Db 602 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 661  
QY 481 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516  
Db 662 GAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 697

RESULT 11  
US-09-944-277A-3/c  
; Sequence 3, Application US/09944277A  
; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect IGE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/944,277A  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1198 nucleotides  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 107..877  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-944-277A-1

Query Match 100.0%; Score 516; DB 9; Length 1198;  
Best Local Similarity 100.0%; Pred. No. 3.4e-157;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-944-277A-3

Query Match  
Best Local Similarity 100.0%; Score 516; DB 9; Length 1198;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 60  
Db GTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 241

61 AATGTGACTCTTACATGTAATCGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120  
Db AATGTGACTCTTACATGTAATCGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 301

121 CACAATGGCAGCCTTTCAAGAGAGACAATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 180  
Db CACAATGGCAGCCTTTCAAGAGAGACAATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 361

181 GAAGCAGTGGAGAGATACAAATGTCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db GAAGCAGTGGAGAGATACAAATGTCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 421

241 CTGGAAGTCTTCAAGTGAAGTCTCTTCAAGTGAAGTCTCTTCAAGTGAAGTCTCTTCAAGT 300  
Db CTGGAAGTCTTCAAGTGAAGTCTCTTCAAGTGAAGTCTCTTCAAGTGAAGTCTCTTCAAGT 481

301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACTGGGATGTGTACAAAGTGAATCTAT 360  
Db CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACTGGGATGTGTACAAAGTGAATCTAT 541

361 TATAAGGATGGTGAAGTCTCTCAAGTGAAGTCTCTCAAGTGAAGTCTCTCAAGTGAAGTCT 420  
Db TATAAGGATGGTGAAGTCTCTCAAGTGAAGTCTCTCAAGTGAAGTCTCTCAAGTGAAGTCT 601

421 GCCACAGTGAAGCAGTGGAACTTACTGTAGCGGCAAGTGTGGCAGCTGGACTAT 480  
Db GCCACAGTGAAGCAGTGGAACTTACTGTAGCGGCAAGTGTGGCAGCTGGACTAT 661

481 GAGTCTGAGCCCTCAACATTTACTGTATAAAAGCT 516  
Db GAGTCTGAGCCCTCAACATTTACTGTATAAAAGCT 697

RESULT 13  
US-10-775-169-141  
; Sequence 141, Application US/10775169  
; Publication No. US20040175743A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael  
; APPLICANT: Twine, Natalie  
; APPLICANT: Dotner, Andrew  
; APPLICANT: Trepicchio, William  
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo  
; FILE REFERENCE: AM101080 (031896-013000)  
; CURRENT APPLICATION NUMBER: US/10/775,169  
; CURRENT FILING DATE: 2004-02-11  
; NUMBER OF SEQ ID NOS: 5278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 141  
; LENGTH: 1198  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-775-169-141

Query Match  
Best Local Similarity 100.0%; Score 516; DB 17; Length 1198;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 60  
Db GTCCCTCAGAAACCTTAAGGTCTCTTGAACCTCCATGGAATAGAAATATTTAAAGGAGAG 241

61 AATGTGACTCTTACATGTAATCGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 120  
Db AATGTGACTCTTACATGTAATCGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTC 301

121 CACAATGGCAGCCTTTCAAGAGAGACAATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 180  
Db CACAATGGCAGCCTTTCAAGAGAGACAATTCAGTTCAGTTCAGTTCAGTTCAGTTCAGTTC 361

181 GAAGCAGTGGAGAGATACAAATGTCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240  
Db GAAGCAGTGGAGAGATACAAATGTCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 421

241 CTGGAAGTCTTCAAGTGAAGTCTCTTCAAGTGAAGTCTCTTCAAGTGAAGTCTCTTCAAGT 300  
Db CTGGAAGTCTTCAAGTGAAGTCTCTTCAAGTGAAGTCTCTTCAAGTGAAGTCTCTTCAAGT 481

301 CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACTGGGATGTGTACAAAGTGAATCTAT 360  
Db CAGCCCTCTTCTCAGTGGCCATGTTGGAGGAACTGGGATGTGTACAAAGTGAATCTAT 541

361 TATAAGGATGGTGAAGTCTCTCAAGTGAAGTCTCTCAAGTGAAGTCTCTCAAGTGAAGTCT 420  
Db TATAAGGATGGTGAAGTCTCTCAAGTGAAGTCTCTCAAGTGAAGTCTCTCAAGTGAAGTCT 601

421 GCCACAGTGAAGCAGTGGAACTTACTGTAGCGGCAAGTGTGGCAGCTGGACTAT 480  
Db GCCACAGTGAAGCAGTGGAACTTACTGTAGCGGCAAGTGTGGCAGCTGGACTAT 661

481 GAGTCTGAGCCCTCAACATTTACTGTATAAAAGCT 516  
Db GAGTCTGAGCCCTCAACATTTACTGTATAAAAGCT 502

RESULT 12  
US-09-962-832-244  
; Sequence 244, Application US/09962832  
; Patent No. US20020110821A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
; FILE REFERENCE: 689290-74  
; CURRENT APPLICATION NUMBER: US/09/962,832  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,077  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,280  
; PRIOR FILING DATE: 2000-09-25  
; NUMBER OF SEQ ID NOS: 259  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 244  
; LENGTH: 1198  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-962-832-244

Query Match  
Best Local Similarity 100.0%; Score 516; DB 9; Length 1198;  
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 302 CACAATGGGAGCCTTTTCAGAGAGACAAATTCAGTTTGAATTCGCAAAATTT 361
Qy 181 GAAGACAGTGGAGATACAAATGTCCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 240
Db 362 GAAGACAGTGGAGATACAAATGTCCAGCACCACCAAGTTAATGAGAGTGAACCTGTGTAC 421
Qy 241 CTGGAAGTCTTTCAGTGAAGTGGTCTCTTCAGGCTCTGCTGAGTGGTGAAGGAGG 300
Db 422 CTGGAAGTCTTTCAGTGAAGTGGTCTCTTCAGGCTCTGCTGAGTGGTGAAGGAGG 481
Qy 301 CAGCCCTCTTCTCAGTGGTCCATGTTGGAGGAACTGGGATGTGTACAAAGTGAATCTAT 360
Db 482 CAGCCCTCTTCTCAGTGGTCCATGTTGGAGGAACTGGGATGTGTACAAAGTGAATCTAT 541
Qy 361 TATAAGATCGTGAAGCTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT 420
Db 542 TATAAGATCGTGAAGCTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT 601
Qy 421 GCCACAGTTGAACAGTGGAACTCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
Db 602 GCCACAGTTGAACAGTGGAACTCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 561
Qy 481 GAGTCTGAGCCCTCAACATTACTGTATAATAAAGCT 516
Db 662 GAGTCTGAGCCCTCAACATTACTGTATAATAAAGCT 697

RESULT 14
US-09-809-715-3
; Sequence 3, Application US/09809715
; Publication No. US2003003502A1
; GENERAL INFORMATION:
; APPLICANT: Jaretzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Wurzburg, Beth A.
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A Fc
; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A Fc REGION OF AN Ige
; TITLE OF INVENTION: ANTIBODY AND USES THEREOF
; FILE REFERENCE: AL-8
; CURRENT APPLICATION NUMBER: US/09/809,715
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,853
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(528)
US-09-809-715-3

Query Match 97.5%; Score 503.2; DB 10; Length 528;
Best Local Similarity 98.4%; Pred. No. 3e-153;
Matches 508; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 60
Db 1 GTCCTCAGAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGAGAG 60
Qy 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGTTCACCAAAATGGTTC 120
Db 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTTGAAGTCAGTTCACCAAAATGGTTC 120
Qy 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATTTGAATGCAAAATTT 180
Db 121 CACAATGGCAGCCCTTTCAGAGAGACAAATTCAGATTTGAATTTGAATGCAAAATTT 180
Qy 181 GAGCAGAGTGGAGATCAATGTGACGACCAACCAAGTTAATGAGAGTGAACCTGTGTAC 240
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Db 181 GAAGACAGTGGAGATACAAATGTCCAGCACCACCAAGTTGCTGAGAGTGAACCTGTGTAC 240
Qy 241 CTGGAAGTCTTTCAGTGAAGTGGTCTCTTCAGGCTCTGCTGAGTGGTGAAGGAGG 300
Db 241 CTGGAAGTCTTTCAGTGAAGTGGTCTCTTCAGGCTCTGCTGAGTGGTGAAGGAGG 300
Qy 301 CAGCCCTCTTCTCAGTGGTCCATGTTGGAGGAACTGGGATGTGTACAAAGTGAATCTAT 360
Db 301 CAGCCCTCTTCTCAGTGGTCCATGTTGGAGGAACTGGGATGTGTACAAAGTGAATCTAT 360
Qy 361 TATAAGATCGTGAAGCTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT 420
Db 361 TATAAGATCGTGAAGCTCTCAAGTACTGTATGAGAACCAACATCTCCATTACAAAT 420
Qy 421 GCCACAGTTGAACAGTGGAACTCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
Db 421 GCCCAGCTGAAGACAGTGGAACTCTACTACTGTACGGGCAAGTGTGGCAGCTGGACTAT 480
Qy 481 GAGTCTGAGCCCTCAACATTACTGTATAATAAAGCT 516
Db 481 GAGTCTGAGCCCTCAACATTACTGTATAATAAAGCT 516

RESULT 15
US-10-434-817-11
; Sequence 11, Application US/10434817
; Publication No. US20030235579A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eric R.
; APPLICANT: McCall, Catherine A.
; TITLE OF INVENTION: NOVEL EQUINE Fc EPSILON RECEPTOR ALPHA
; TITLE OF INVENTION: CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/434,817
; FILING DATE: 08-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,734
; FILING DATE: 29-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1...603
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-434-817-11

Query Match 55.7%; Score 287.2; DB 16; Length 603;
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Best Local Similarity 77.2%; Pred. No. 1.1e-82;  
Matches 349; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

Qy	7	CAGAAACCTTAAGTCTCTTGAACCTCCATGGAATGAATATTTAAAGGAGAGAAATGTG	66
Db	82	CGAAATCTACAGTCTCTTGAATCCCATGGAATGAATATTTGAGGAGAGAAATGTG	141
Qy	67	ACTTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCACCAAAATGGTTCACAAT	126
Db	142	ACTCTTACATGTAATAAGACAAGCCCTTAAAGGCAACTCCACTGAGTGGACCTACAAC	201
Qy	127	GCACCCCTTCAGAGAGACAAATTCAGTTTGAATTTGATGCAAAATTTGAAGAC	186
Db	202	AACACCCTTTAGAAGTGACAACTTCAAGTTTGAACATCACTAATGCTCTCACCCGAGC	261
Qy	187	AGTGAGAGATACAAATGTGACACCACCAACAAGTTAATGAGAGTGAACCTGTGTACTGGAA	246
Db	262	AGTGGGAATACAGATGTCGGAACAATGACTTGAACCTGAGTGAAGCTGTGCACCTAGAA	321
Qy	247	GTCCTCAGTGACTGCTGCTCTTTCAGSCCTCTGCTGAGGTGGTGAAGGGGCCAGCCC	306
Db	322	GTCTTCAGTGACTGCTGCTCTTTCAGSCCTCTGCTGAGGAGGTCTAGAGGGTAAAGGCC	381
Qy	307	CTCTTCTCAGTGCCATGGTTGGAGAACTGGGATGTGTACAAGGTGATCTATTATAAG	366
Db	382	CTCGTTCTCAGGTGCGGTGGTGGAGGATTGGGACGCTTCAAGGTGAICTACTACAAG	441
Qy	367	GATGTGAAGTCTCAAGTACTGGTATGAGAACCAACAATCTCCATTACAATGCCACA	426
Db	442	GATGCCAAACCCCTCGAGTACTGTGTATGAGAACAAAACATCTCCATTGAAAGTGCCACA	501
Qy	427	GTGGAAGACAGTGGAACTTACTGTACGGG	458
Db	502	ACAGAAAACAGTGGCACCTATTACTGGAGGG	533

Search completed: October 11, 2004, 01:41:42  
Job time : 301.613 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 1741.12 Seconds  
(without alignments)  
8849.962 Million cell updates/sec

Title: US-10-763-400-12

Perfect score: 516  
Sequence: 1 gccctcagaacctaaagt.....acattactgtataaaagct 516

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues  
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*  
2: em\_estum.\*  
3: em\_estin.\*  
4: em\_estmu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_esti.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_phg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gss1.\*  
29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	507.2	98.3	810	12	BG542554
2	492	95.3	834	10	BF679057
3	434.8	84.3	840	12	BG548515
4	420.2	81.4	760	12	BG542157

5 406.2 78.7 845 10 BF678252  
6 333.6 64.7 818 10 BF677190  
7 294 57.0 768 13 BQ573778  
8 293.6 56.9 660 14 CF362072  
9 250.8 48.6 652 13 BY752906  
10 234 45.3 707 14 CA448745  
11 228.6 44.3 712 14 CA419024  
12 218.6 41.2 394 10 AW357271  
13 198.8 38.5 669 10 AW612525  
14 178.2 34.5 422 10 BF603113  
15 175.6 34.0 403 14 CB768694  
16 169 32.8 848 14 CB958187  
17 167.8 32.5 1033 9 AL549464  
18 167.8 32.5 1201 9 AL531122  
19 166.2 32.2 874 14 CD244088  
20 166.2 32.2 1201 9 AL514096  
21 166.2 32.2 1201 13 BX399366  
22 163 31.6 823 12 BI768140  
23 161.4 31.3 987 13 BX345202  
24 161.4 31.3 1201 13 BX402696  
25 158.8 31.0 664 14 CB55672  
26 159.4 30.9 651 14 CF363368  
27 159 30.8 852 12 BI821954  
28 156.6 30.3 528 14 CB152997  
29 154.8 30.0 571 14 CD693938  
30 154.6 30.0 640 9 AU137840  
31 153.6 29.8 1201 9 AL558081  
32 150.6 29.2 429 13 BY228345  
33 148.8 28.8 551 12 BM364531  
34 148.8 28.1 270 10 AW357272  
35 143.6 27.8 812 13 BX378677  
36 143.4 27.8 615 12 BM991911  
37 141.8 27.5 411 10 BF902392  
38 141.4 27.4 678 14 CB483332  
39 140.8 27.3 403 13 BY228552  
40 140.8 27.3 404 13 BY227642  
41 140 27.1 373 13 BY041924  
42 139 26.9 520 14 CB537050  
43 138.6 26.9 449 10 BF932877  
44 138.6 26.9 449 10 BF933349  
45 137.2 26.6 1060 9 AL570702

#### ALIGNMENTS

RESULT 1  
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LOCUS 602572052F1 NIH\_MGC\_77 Homo sapiens CDNA clone IMAGE:4696381 5',  
DEFINITION mRNA sequence.  
ACCESSION BG542554  
VERSION BG542554.1 GI:13534787  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 810)  
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLC1523 row: h column: 14  
High quality sequence stop: 667.

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CA419024 UI-H-E21-  
AW357271 40240 MAR  
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BF603113 288539 MA  
CB768694 AMGNNUC:S  
CB958187 AGENCOURT  
AL549464 AL549464  
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CD244088 AGENCOURT  
AL514096 AL514096  
BX399366 BX399366  
BI768140 603056571  
BX345202 BX345202  
BX402696 BX402696  
CB55672 MMSPO057  
CF363368 831220 MA  
BI821954 603039767  
CB152997 K-EST0210  
CD693938 EST10461  
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AL558081 AL558081  
BY228345 BY228345  
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## FEATURES

source

## Location/Qualifiers

1. 810  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="IMAGE:4696381"  
 /lab host="DH10B (T1 phage-resistant)"  
 /clone lib="NIH MGC 77"  
 /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 98.3%; Score 507.2; DB 12; Length 810;  
 Best Local Similarity 99.4%; Pred. No. 8e-138;  
 Matches 509; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGATAGAAATTTAAAGGAGAG 60  
 DB 106 GTCCCTCAGAACCTTAAGTCTCTTGAACCTCCATGGATAGAAATTTAAAGGAGAG 165

QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 120  
 DB 166 AATGTGACTCTTACATGTAATGGGAACAATTTCTTGAAGTCAGTTCACCAATGGTTC 225

QY 121 CACAATGCGACGCTTTTCAAGAGAGACAAATTCAAAGTTTGAATATTTGTAATGCCAAATTT 180  
 DB 226 CACAATGCGACGCTTTTCAAGAGAGACAAATTCAAAGTTTGAATATTTGTAATGCCAAATTT 285

QY 181 GAAGACAGTGGAGAAATACAAATGTCAGCACCAACAAAGTAAATGAGAGTGAACCTGTGTAC 240  
 DB 286 GAAGACAGTGGAGAAATACAAATGTCAGCACCAACAAAGTAAATGAGAGTGAACCTGTGTAC 345

QY 241 CTGGAAGTCTTTCAGTACTGGCTCTCTTCAAGCCCTCTGCTGAGGTTGGTGTATGAGAGGC 300  
 DB 346 CTGGAAGTCTTTCAGTACTGGCTCTCTTCAAGCCCTCTGCTGAGGTTGGTGTATGAGAGGC 405

QY 301 CAGCCCTCTTTCAGTACTGGCTCTCTTCAAGCCCTCTGCTGAGGTTGGTGTATGAGAGGC 360  
 DB 406 CAGCCCTCTTTCAGTACTGGCTCTCTTCAAGCCCTCTGCTGAGGTTGGTGTATGAGAGGC 465

QY 361 TATAAGGATGTTGAAGTCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
 DB 466 TATAAGGATGTTGAAGTCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 525

QY 421 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTGTGGAGCTGGACTAT 480  
 DB 526 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAGTGTGGAGCTGGACTAT 585

QY 481 GAGTCTGAGCCCTCAACATTACTGTATAAAA 512  
 DB 586 GAGTCTGAGCCCTCAACATTACTGTATAAAA 617

## RESULT 2

BF679057

LOCUS

DEFINITION 602153315F1 NIH\_MGC\_83 Homo sapiens cDNA clone IMAGE:4294467 5', mRNA sequence.

ACCESSION

BF679057

VERSION

BF679057.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 834)

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgs.mci.nih.gov/>  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: CLONETECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCM1143 row: n column: 04  
 High quality sequence stop: 621.

Location/Qualifiers

1. 834

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4294467"

/lab host="DH10B (T1 phage-resistant)"

/clone lib="NIH MGC 83"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

Source

1. 834

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4294467"

/lab host="DH10B (T1 phage-resistant)"

/clone lib="NIH MGC 83"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

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1. 834

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

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/lab host="DH10B (T1 phage-resistant)"

/clone lib="NIH MGC 83"

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1. 834

/organism="Homo sapiens"

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/db\_xref="taxon:9606"

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/lab host="DH10B (T1 phage-resistant)"

/clone lib="NIH MGC 83"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

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/db\_xref="taxon:9606"

/clone="IMAGE:4294467"

/lab host="DH10B (T1 phage-resistant)"

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/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4294467"

/lab host="DH10B (T1 phage-resistant)"

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/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

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1. 834

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4294467"

/lab host="DH10B (T1 phage-resistant)"

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1. 834

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4294467"

/lab host="DH10B (T1 phage-resistant)"

/clone lib="NIH MGC 83"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

Source

1. 834

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4294467"

/lab host="DH10B (T1 phage-resistant)"

/clone lib="NIH MGC 83"

/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattatgcc); Site 2: SfiI (ggccattatgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

Db 585 GAGTCTGAG-CCTCAACATTACTGTAAATAAAGCT 619

|||||

RESULT 3  
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 DEFINITION mRNA sequence.

ACCSSION  
 BG548515 1 GI:13547180  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)

REFERENCE  
 1 (bases 1 to 840)  
 NIH-MGC <http://mgc.nci.nih.gov/>,  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 EMAIL: [cgapbs-x@mail.nih.gov](mailto:cgapbs-x@mail.nih.gov)  
 TISSUE Procurement: CLONTECH Laboratories, Inc.  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1CM1544 row: p column: 01  
 High quality sequence stop: 590.  
 Location/Qualifiers

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 SfiI (ggcgctcgcc); Site 2: SfiI (ggcgctatggcc); 5' and  
 3' adaptors were used in cloning as follows: 5' adaptor  
 sequence: 5'-CACGGCATATGGCG-3', and 3' adaptor sequence:  
 5'-ATTCTAGACGCGGCGGCACATG-dt(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.9  
 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 84.3%; Score 434.8; DB 12; Length 840;  
 Best Local Similarity 96.9%; Pred. No. 1.7e-116;  
 Matches 465; Conservative 0; Mismatches 12; Indels 3; Gaps 2;

QY 1 GTCCTCAGAAACCTTAAGGTCCTCCTTGAAACCTCCATGGATAGATAATTTAAAGGAGAG 60  
 DB 106 GTCCTCAGAAACCTTAAGGTCCTCCTTGAAACCTCCATGGATAGATAATTTAAAGGAGAG 165

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QY 181 GAAGACAGTGGAGAAATCAAAATGTACAGCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
 DB 286 GAAGACAGTGGAGAAATCAAAATGTACAGCAACAAAGTTAATGAGAGTGAACCTGTGTAC 345

QY 241 CTGGAAGCTTTCAGTGAAGTGTCTCTCTTCTGAGGCTCTGTGAGTGGTGTATGAGGGC 300

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Qy	272	AGGCCTCTGCTGAGTGGTGTATGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGA	331	
Db	278	AGGCCTCTGCTGAGTGGTGTATGAGGGCCAGCCCTCTTCTCAGGTGCCATGTTGGA	337	
Qy	332	GGAACTGGATGTGTAACAAGTGTATCTATTATATAGGATGGTGAAGCTCTTCAAGTACTGGT	391	
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Qy	392	ATGAGAACCCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGATGGGAACCTACTACT	451	
Db	398	ATGAGAACCCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGATGGGAACCTACTACT	457	
Qy	452	GTACGGGCAAGTGTGGCAGCTGACCTATGAGTCTGAGCCCTCAACATTAATAA	511	
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VERSION	BF678252.1 GI:11952147			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	1 (bases 1 to 846)			
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .			
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabs-k@mail.nih.gov">cgabs-k@mail.nih.gov</a> Tissue Procurement: CLONTECH Laboratories, Inc. CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLCMI071 row: j column: 15 High quality sequence stop: 609. Location/Qualifiers 1. .846 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4250222" /lab_host="DH10B (T1 phage-resistant)" /clone_lib="NIH_MGC_83" /note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site 1: SfII (ggcgccctggcc); Site 2: SfII (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGGGCCATTATGGCC-3', and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 Kb (range 0.5-4.0 Kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."			
FEATURES	source			
ORIGIN				

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Site 1: SfiI (ggcgctcgcc); Site 2: SfiI  
(ggcattatgcc); 5' and 3' adaptors were used in cloning  
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCCC-3'  
and 3' adaptor sequence:  
5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.4  
kb (range 0.5-4.0 kb). 14/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA)."
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## ORIGIN

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Query Match 64.7%; Score 333.6; DB 10; Length 818;  
Best Local Similarity 89.6%; Pred. No. 1e-86;  
Matches 473; Conservative 0; Mismatches 39; Indels 16; Gaps 10;  
  
QY 1 GTCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAG 60  
Db 110 GTCCTCAGAACTTAAGTCTCTTGAACCTCCATGGAATAGATATTTAAAGGAG 169  
  
QY 61 AATGTGACTCTTACATGTAATGGGAACAATTTCTT-TGAAGTCAGTTCCACCAATGGTT 119  
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Db 290 AATGTGAGACAGTGGAGAA--ACAATGTGAGCAGCAACAAAGTTAATGAGTGAAC 349  
  
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QY 352 GTGATCTATTATAGGATGTGAAGTCTCAAGTACTGTATGAGAACCAACATCTCC 411  
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QY 412 ATTACAAATGCCAGTTGAAGACAGTGGAAAC---TACTACTGTAGCGGCAA-CTGTG 467  
Db 528 ATTACAAATGCCAGTGGAAAGACAGGGGGAACCTAACTACTTGTACGGGCAAGGTGTG 587  
  
QY 468 GCAGCTGACTA-TGACTCTGAGCCCTCAACATTACTGTAAATAAAG 514  
Db 588 GCAGTGGACTATTGACTCTTGAGCCCTCAACATTAGTGTAAATAAAG 635
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## RESULT 7

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B0573778/c  
LOCUS B0573778 768 bp mRNA linear EST 19-JUN-2002  
DEFINITION UI-H-EZO-bav-1-04-0-UI.s1 NCI CGAP Ch1 Homo sapiens CDNA clone  
B0573778  
ACCESSION B0573778  
VERSION B0573778.1 GI:21477095  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 768)  
REFERENCE  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
```

JOURNAL  
COMMENT

```
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: ccapbs@mail.nih.gov  
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of  
Orthopaedics  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, bento-soares@uiowa.edu  
The following repetitive elements were found in this cDNA  
sequence: 1-41, >Alu_richlow.complexity (matched complement)  
93-129, >LINE2 (matched complement)  
Seq primer: M13 FORWARD  
POLYA=Yes.
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## FEATURES

## Location/Qualifiers

## source

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/mol_type="mRNA"  
/db_xref="taxon:9606"  
/clones="UI-H-EZO-bav-1-04-0-UI"  
/tissue_type="Chondrosarcoma Grade II"  
/dev_stage="Adult"  
/lab_host="DH10B (Life Technologies)"  
/clone_lib="NCI-CGAP Ch1"  
/note="Organ: Left Pelvis; Vector: p773-Pac (Pharmacia)  
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP Ch1 is a cDNA library containing the following  
tissue(s): Chondrosarcoma Grade II. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into p773-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
dT18 tail. The sequence tag for this library is  
TGATCAGCT.  
TAG_TISSUE=grade-2-chondrosarcoma  
TAG_LIB=UI-H-EZO  
TAG_SEQ=ATCTAATATG"
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## ORIGIN

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Query Match 57.0%; Score 294; DB 13; Length 768;  
Best Local Similarity 99.7%; Pred. No. 4.5e-75;  
Matches 294; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 222 TGAGAGTGAACCTGTGTACTCTGGAAGTCTTCAGTGACTGGTCTCTCAGGCTCTGCG 281  
Db 768 TGAGAGTGAACCTGTGTACTCTGGAAGTCTTCAGTGACTGGTCTCTCAGGCTCTGCG 709  
  
QY 282 TGAGGTGTGATGGAGGCCAGCCCTCTTCTCAGTGGCCATGGTTGAGGAACTGGGA 341  
Db 708 TGAGGTGTGATGGAGGCCAGCCCTCTTCTCAGTGGCCATGGTTGAGGAACTGGGA 649  
  
QY 342 TGGTGTACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCA 401  
Db 648 TGGTGTACAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCA 589  
  
QY 402 CAACATCTCCATTACAAATGCCACAGTTCAAGACAGTGGAACTTACTACTGTACGGGCAA 461  
Db 588 CAACATCTCCATTACAAATGCCACAGTTCAAGACAGTGGAACTTACTACTGTACGGGCAA 529  
  
QY 462 AGTGTGGCAGCTGGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516  
Db 528 AGTGTGGCAGCTGGGACTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 474
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## RESULT 8

## CF362072

## LOCUS

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CF362072 660 bp mRNA linear EST 25-AUG-2003
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DEFINITION 828457 MARC 3P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION CF362072
VERSION CF362072.1 GI:34161364
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa

REFERENCE
AUTHORS Smith, T.P.L., Freking, B.A., Ford, J.J., Valliet, J.L., Fox, J., Wise, T.A., Nomenan, D.J., Wray, J.E. and Keele, J.W.
TITLE A second set of porcine ESTs from a pooled-tissue normalized library
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: SRG8018 row: L column: 4
Seq primer: GTAATACGACTCACTATAGGG.
FEATURES
source
location/Qualifiers
1..660
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/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3P1G"
/notes="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including brain, liver, muscle, placenta/endometrium, ovary, testes, and bone marrow."

ORIGIN
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Best Local Similarity 73.1%; Pred. No. 5.3e-75;
Matches 377; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 1 GTCCTCAGAAACCTAGTCTCTTGAACCTCCATGGAATGAGATATTAAAGGAG 60
Db |||
QY 91 GTCATCCAGGAATCTCAGGTGTCCTTGAATCCCTCCATGGAATGGAATTTAGAGGAG 150
Db |||
QY 61 AATGTGACTCTTACATGTAATGGGAACTTCTTGAAGTCAGTCCACCAATGGTTC 120
Db |||
QY 151 AATGTGACTCTCAGTATGGAAGTGGACGATGCCCTTGAAATTTACCCCAATTTGACA 210
Db |||
QY 121 CACAAATGGAGCCCTTCAGAGAGACAAATCAAGTTTGAATATTTGTAATGCCAAATTT 180
Db |||
QY 211 CACAAACAAACAACTTTGGAAGTGGAACTTCGAGTGGACCTTAAGAAATGCAAAACCT 270
Db |||
QY 181 GAGACAGTGGAGATACAAATGTCAGCACAACAGTTAATGAGAGTGAACCTGTGAC 240
Db |||
QY 271 GGGGACAGCGCAATACAGATGCCAAGCAAGACTTTTCAATGAGTGAACCTGTGCAC 330
Db |||
QY 241 CTGGAAGTCTTCAAGTACTGGCTGCTCTTCAGGCCCTCTGCTGAGGTGGTGTGAGGGGC 300
Db |||
QY 331 CTAGAAGTCAATCAGTACTGGCTGCTCTTCAGACCTCTGTCCCGGTGGTGGGAAGGC 390
Db |||
QY 301 CAGCCCTCTTCTCAGTGGCCATGGTTGAGAGAACTGGGATGTGTACAGGTGATCTAT 360
Db |||
QY 391 CAGTCTCTCTCTCAGTGTGTCAGCGTGGGAAGAACTGGAATGCTTATAGGTGATCTAC 450
Db |||
QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420
Db |||
QY 451 TACAAGGATGCCAAGCCCTCAAGTACTGGTATGAGAACCAACCTCTCCATTACCAAT 510
Db |||
QY 421 GCACAGTTGAAGACAGTGGAACTTACTGTAATGACGGGAAGAGTGGCAGCTGGACTAT 480
Db |||

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828457 MARC 3P1G Sus scrofa cDNA 5', mRNA sequence.  
 CF362072  
 CF362072.1 GI:34161364  
 EST.  
 Sus scrofa (pig)  
 Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 1 (bases 1 to 660)  
 Smith, T.P.L., Freking, B.A., Ford, J.J., Valliet, J.L., Fox, J., Wise, T.A., Nomenan, D.J., Wray, J.E. and Keele, J.W.  
 A second set of porcine ESTs from a pooled-tissue normalized library  
 Unpublished (2003)  
 Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified with cross\_match v0.990329.  
 Plate: SRG8018 row: L column: 4  
 Seq primer: GTAATACGACTCACTATAGGG.  
 Location/Qualifiers  
 1..660  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
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 /clone\_lib="MARC 3P1G"  
 /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including brain, liver, muscle, placenta/endometrium, ovary, testes, and bone marrow."

Query Match 56.9%; Score 293.6; DB 14; Length 660;  
 Best Local Similarity 73.1%; Pred. No. 5.3e-75;  
 Matches 377; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

1 GTCCTCAGAAACCTAGTCTCTTGAACCTCCATGGAATGAGATATTAAAGGAG 60  
 91 GTCATCCAGGAATCTCAGGTGTCCTTGAATCCCTCCATGGAATGGAATTTAGAGGAG 150  
 61 AATGTGACTCTTACATGTAATGGGAACTTCTTGAAGTCAGTCCACCAATGGTTC 120  
 151 AATGTGACTCTCAGTATGGAAGTGGACGATGCCCTTGAAATTTACCCCAATTTGACA 210  
 121 CACAAATGGAGCCCTTCAGAGAGACAAATCAAGTTTGAATATTTGTAATGCCAAATTT 180  
 211 CACAAACAAACAACTTTGGAAGTGGAACTTCGAGTGGACCTTAAGAAATGCAAAACCT 270  
 181 GAGACAGTGGAGATACAAATGTCAGCACAACAGTTAATGAGAGTGAACCTGTGAC 240  
 271 GGGGACAGCGCAATACAGATGCCAAGCAAGACTTTTCAATGAGTGAACCTGTGCAC 330  
 241 CTGGAAGTCTTCAAGTACTGGCTGCTCTTCAGGCCCTCTGCTGAGGTGGTGTGAGGGGC 300  
 331 CTAGAAGTCAATCAGTACTGGCTGCTCTTCAGACCTCTGTCCCGGTGGTGGGAAGGC 390  
 301 CAGCCCTCTTCTCAGTGGCCATGGTTGAGAGAACTGGGATGTGTACAGGTGATCTAT 360  
 391 CAGTCTCTCTCTCAGTGTGTCAGCGTGGGAAGAACTGGAATGCTTATAGGTGATCTAC 450  
 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACATCTCCATTACAAAT 420  
 451 TACAAGGATGCCAAGCCCTCAAGTACTGGTATGAGAACCAACCTCTCCATTACCAAT 510  
 421 GCACAGTTGAAGACAGTGGAACTTACTGTAATGACGGGAAGAGTGGCAGCTGGACTAT 480

DEFINITION 828457 MARC 3P1G Sus scrofa cDNA 5', mRNA sequence.  
 ACCESSION CF362072  
 VERSION CF362072.1 GI:34161364  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa

REFERENCE  
 AUTHORS Smith, T.P.L., Freking, B.A., Ford, J.J., Valliet, J.L., Fox, J., Wise, T.A., Nomenan, D.J., Wray, J.E. and Keele, J.W.  
 TITLE A second set of porcine ESTs from a pooled-tissue normalized library  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified with cross\_match v0.990329.  
 Plate: SRG8018 row: L column: 4  
 Seq primer: GTAATACGACTCACTATAGGG.

RESULT 9  
 BY752906  
 LOCUS  
 DEFINITION  
 cDNA clone F930034C11 5', mRNA sequence.

Db 511 GCCAAAAGAGAGACAGTGGCTCTTATTGGTGCACGGGCATTAATTCAAAAAATACCAAAA 570

QY 481 GAGTCTGAGCCCTCAACATTACTGTGTAATAAAGCT 516

Db 571 AACTCTACTCTCTCACCATTACCAACACAGAT 606

BY752906 652 bp mRNA linear EST 17-DEC-2002  
 BY752906 RIKEN full-length enriched, adult inner ear Mus musculus  
 cDNA clone F930034C11 5', mRNA sequence.  
 BY752906  
 BY752906.1 GI:27184082  
 EST.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 652)

REFERENCE  
 AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baidarelli, R., Hill, D.P., Sult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Bruscia, V., Chothia, C., Corbani, L.E., Cousins, S., Della, B., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, I., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wyszewski, B., Yang, Y., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, I., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 22354683  
 12466851

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-2 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@sc.riken.go.jp  
 URL: http://genome.ssc.riken.go.jp/  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in Riken.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Tissues were provided by Kirk W. Beisel ( Boys Town National  
 Research Hospital 535 North 30th Street Omaha, NE 68131 USA ) whose  
 assistance we gratefully acknowledge.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.

## FEATURES

source

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1..652
/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="F930034C11"
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## ORIGIN

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Query Match      48.6%; Score 250.8; DB 13; Length 652;
Best Local Similarity 70.3%; Pred. No. 2.1e-62;
Matches 365; Conservative 0; Mismatches 148; Indels 6; Gaps 2;

QY 1 GPCCTCGAAGACCTTAAGGTCTCTTGAACCTCCATCGAATGAATATTAAGGAGAG 60
DB 102 GCCATCGAATCTGTACTACCTTGGACCCACATGGATTAGATATTACAGAGAG 151
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DB 162 AAAGTGACCTTCTCTGTCTGGAACAAATCACCTTCAAAATGAACCTACTACTAAATGG 221
QY 118 TTCCACATGCGAGCTTTTCAGAGAGACAAATTCAGTTTGAATTTGTAATGGATGCCAA 177
DB 222 ATCCAAATGTTACCGTCTCTGAGTGAACTCTTCATTTGGTCATTTGAGTGGCACC 281
QY 178 TTGAAGACAGTGGAGATAAATATGTCAGACCAACAAAGTTAATGAGAGTGAACCTGTG 237
DB 282 GTTCAAGACAGTGGAAATACATATGTCAGAAAGCAAGATTTGTTAAGAGTAAACCTGTG 341
QY 238 TACCTGGAAGCTTCAGTGACTGCTCTCTCTCAGGCCTCTGCTGAGGTGGTGTGAGGAG 297
DB 342 TACTTGAATGTAAAGCAAGATTGGCTGCTCTCTCAGACATCTGCTGACATGATCTTAGTC 401
QY 298 GGCCAGGCCCTCTTCTCAGTGCCATGTTGGAGGAACCTGGATGTTACAAAGGTGATC 357
DB 402 CATGGATCCTTTGACATCAGATGCCATGGCTGGGAAGAACTGGAATGTCGCAAGGTGATC 461
QY 358 TATTATAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACACATCTCCATTACA 417
DB 462 TACTACAGAAATGACCATGCTTTCACTACAGATTATGAGAGCC---CCGTCCTCCATTAGA 518
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QY 478 TATGAGTCTGAGCCCTCAACATTTACTGTATATAAAGCT 516
DB 579 TATGAATCTGACAAATTCAGAAATTCGTTAGTAAAGCT 617

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RESULT 10

CA448745/c

LOCUS

707 bp mRNA linear

EST 08-NOV-2002

CA448745

## DEFINITION

UI-H-E10-ayo-p-24-0-UI.s1 NCI CGAP E10 Homo sapiens cDNA clone  
 UI-H-E10-ayo-p-24-0-UI 3', mRNA sequence.

## ACCESSION

CA448745

## VERSION

CA448745.1

## KEYWORDS

EST.

## SOURCE

Homo sapiens

## ORGANISM

Homo sapiens (human)

## REFERENCE

1 (bases 1 to 707)

## AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, [bento-soares@iowa.edu](mailto:bento-soares@iowa.edu)  
 The following repetitive elements were found in this cDNA  
 sequence: 93-129, >LINE2 (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1..707

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/db\_xref="taxon:9606"

/clone="UI-H-E10-ayo-p-24-0-UI"

/tissue\_type="Chondrosarcoma"

/dev stage="Adult"

/lab\_host="DH10B (Life Technologies)"

/clone\_lib="NCI-CGAP-E10"

/note="Organ: Left pelvis; Vector: pT73-Pac (Pharmacia)  
 with a modified polylinker; Site 1: EcoR I; Site 2: Not I;  
 NCI CGAP E10 is a cDNA library containing the following  
 tissue(s): Chondrosarcoma. The library was constructed  
 according to Bonaldo, Lennon and Soares, Genome Research,  
 6:791-806, 1996. First strand cDNA synthesis was primed  
 with an oligo-dT primer containing a Not I site. Double  
 stranded cDNA was ligated to an EcoR I adaptor, digested  
 with Not I, and cloned directionally into pT73-Pac  
 vector. The oligonucleotide used to prime the synthesis of  
 first-strand cDNA contains a library tag sequence that is  
 located between the Not I site and the (dr)18 tail. The  
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 TAG\_TISSUE=chondrosarcoma  
 TAG\_LIB=UI-H-E10  
 TAG\_SEQ=ACACTTGCAC"

## ORIGIN

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Query Match      45.3%; Score 234; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 1.9e-57;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 707 GAGTGTGTATGAGGGCCAGCCCTCTTCTCAGTGGCATGTTGGAGGAACCTGGAT 648
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DB 647 GTGTACAAAGGTGATCTATTATAGGATGGTGAAGCTCTCAAGTACTGCTATGAGAACCAC 588
QY 403 AACATCTCCATTCAAAATGCCAGTTGAAGACAGTGGAACTTACTTGTACGGCAAA 462
DB 587 AACATCTCCATTCAAAATGCCAGTTGAAGACAGTGGAACTTACTTGTACGGCAAA 528
QY 463 GTGTGGCAGCTGGACTATGATCTGAGCCCTCAACATTACTCTATAAAGCT 516
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```

RESULT 11
CA419024/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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UI-H-E21-bbj-e-19-0-UI-s1 NCI CGAP Ch2 Homo sapiens cDNA clone
UI-H-E21-bbj-e-19-0-UI 3', mRNA sequence.
CA419024
CA419024.1 GI:24781675
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 712)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
Orthopaedics
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-42, >(TAAA)nSimple_repeat (matched complement)
94-130, >LINE2, (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..712
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-E21-bbj-e-19-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev stage="Adult"
/lab host="DH10B (Life Technologies)"
/clone lib="NCI CGAP Ch2"
/note="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCTT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-E21
TAG_SEQ=ATCTAATATG"

ORIGIN
Query Match 44.3%; Score 228.6; DB 14; Length 712;
Best Local Similarity 97.1%; Pred No. 7.6e-56;
Matches 231; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 279 TGCTAGGTGGTATGAGGCGCCAGCCCTCTTCCTCAGTGCCATGGTTGGAGGAATG 338
Db 712 TGCTAGGTGGTATGAGGCGCCAGCCCTCTTCCTCAGTGCCATGGTTGGAGGAATG 653
QY 339 GGATGTGTACAGGTATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGCTATGAGAA 398
Db 652 GGATGTGTACAGGTATCTATTATTAAGGATGGTGAAGCTCTCAAGTACTGCTATGAGAA 593

399 CCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGG 458
592 CCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACTACTACTGTACGGG 533
459 CAAAGTGTGGCAGCTGGAGCTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 516
532 CAAAGTGTGGCAGCTGGAGCTATGAGTCTGAGCCCTCAACATTACTGTAAATAAAGCT 475

RESULT 12
AW357271
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

394 bp mRNA linear EST 25-APR-2001
40240 MARS 2BOV Bos taurus cDNA 5', mRNA sequence.
AW357271
AW357271.1 GI:6861277
EST.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 394)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.M., Rohrer, G.A.,
Chitko-McKown, C.G., Pettea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.
Sequence evaluation of four pooled tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the "minscore 20
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
Plate: 18 row: C column: 5
Seq primer: ATTGAGTGACACTATAG.
Location/Qualifiers
1..394
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab host="DH10B"
/clone lib="MARS 2BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."

ORIGIN
Query Match 41.2%; Score 212.6; DB 10; Length 394;
Best Local Similarity 73.3%; Pred No. 2.6e-51;
Matches 272; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 9 GAAACCTAAGTCTCTTGAACCCCTCCATGGAATAGATATTTAAAGGAGAGAAATGTGAC 68
Db 24 GAAATCTAAGGTGTCCTTTGAATCCACCATGGAGAAAATACTTTAAAGGAGATGCTGTGAC 83
QY 69 TCCTTACATGTAATGGGAGCAATTTCTTTGAAGTCAGTTCACCACCAATGTTCCCAATGG 128
Db 84 TCCTTACATGTAAGTACGAAACGGTTCCTCTGAAGACCAAGTCTCTCTGTGGATCCCAATGG 143

```



QY 129 CAGCTTTTCAGAGAGACAAATTCAGTTGATATATGTAATGCGCAATTTGAGAGACAG 188  
 DB 144 AACAGATTTCACAGATATATTCAGATGCGCAATTTGTAAGAGCAGCATGCGAGACAG 203  
 QY 189 TGGAGATACAAATGTCAGACCAACAAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGT 248  
 DB 204 TGGGGAATACCAATGCCGAATCAAGGATTTGCCATCAGTGAACCCGTATACCTAATGT 263  
 QY 249 CTTAGTACACTGGTGTCTCTTCAGGCTCTCTGAGGCTGTCTGAGGCTGTGATGAGGCGCCCT 308  
 DB 264 CATCAGTACACTGGTGTATCATTCAGGCTCTCTGAGGCTGTGATGAGGCTGTGAGTCCCT 323  
 QY 309 CTTCTCAGTGGCCATGTTGGAGGAACTGGGATGTGTACAAAGTGTATCTATTATAAGGA 368  
 DB 324 CTTCTCAGTGGCCACAGTGGAGAAATCTGAATGCTTCAGGCTGTATCTACTACAAGGA 383  
 QY 369 TGGTGAAGCTC 379  
 DB 384 TAACAAGCTC 394

RESULT 13  
 LOCUS AW612525 669 bp mRNA linear EST 23-MAR-2000  
 DEFINITION hh03f07.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2954053 3',  
 similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR  
 ALPHA-SUBUNIT (HUMAN); mRNA sequence.  
 ACCESSION AW612525  
 VERSION  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 669)  
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 NCI-CGAP National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strauberg, Ph.D.  
 Email: cgaaps-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 DNA Library Arrayed by: Greg Lennon, Ph.D.  
 Cloning Distribution: Washington University Genome Sequencing Center  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 image.llnl.gov/image/html/iresources.shtml  
 Seg primer: -40up from Gibco  
 High quality sequence stop: 438.

FEATURES  
 source  
 1..669  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2954053"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Kid11"  
 /note="Organ: kidney; Vector: p773D-Pac (Pharmacia) with  
 a modified polylinker; Site1: Not I; Site2: Eco RI;  
 Plasmid DNA from the normalized library NCI CGAP Kid3 was  
 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (clones 1322376-1323911, 1456007-1456775, and  
 1500552-1502855). Subtraction by Bento Soares and M.  
 Fatima Bonaldo.

ORIGIN  
 Query Match 38.5%; Score 198.8; DB 10; Length 669;  
 Best Local Similarity 96.2%; Pred. No. 4.3e-47;

Matches 203; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 306 CCTCTTCTCCTCAGGTGCGATGTTGGAGAACTGGGATGTGTACAAAGTGTATTTATAA 365  
 DB 669 CCTCTTCTCCTCAGGTGCGATGTTGGAGAACTGGGATGTGTACAAAGTGTATTTATAA 610  
 QY 366 GGATGGTGAAGTCTCAAGTACTGGTATGAGACCAACACATCTCCATTACAAATGCCAC 425  
 DB 609 GGATGGTGAAGTCTCAAGTACTGGTATGAGACCAACACATCTCCATTACATATGCCAC 550  
 QY 426 AGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCACTGGCAATATGAGTC 485  
 DB 549 AGTTGAAGACAGTGGAACTTACTGTACGGGCAAGTGTGGCACTGGCAATATGAGTC 490  
 QY 486 TGAGCCCTCAACATTTACTGTATAAAGCT 516  
 DB 489 TGAGCCCTCAACATTTACTGTATAAAGCT 459

RESULT 14  
 LOCUS BF603113 422 bp mRNA linear EST 25-APR-2001  
 DEFINITION 28539 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
 ACCESSION BF603113  
 VERSION BF603113.1 GI:11700395  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 1 (bases 1 to 422)  
 TITLE Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
 Casas, E., Wray, J.E., White, J., Cho, J., Fahrkrug, S.C.,  
 Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,  
 Chitko-Mckown, C.G., Bertha, G., Holt, I., Karamycheva, S., Liang, F.,  
 Quackenbush, J., and Keesle, J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine cDNA  
 libraries and construction of a gene index for cattle  
 Genome Res. 11 (4), 626-630 (2001)

JOURNAL 21180013  
 MEDLINE 11282978  
 PUBMED  
 COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called and alt trimmed with phred  
 v0.980904.e. Vector identified by cross\_match with the -minscore 18  
 and -mismatch 12 options.  
 PCR Primers  
 FORWARD: AGGAACACGCTATGACCAT  
 BACKWARD: GTTTCCTCCAGTCACGACG  
 Plate: 47 row: N Column: 12  
 Seq primer: ATTAGGTGACACTATAG.

FEATURES  
 Location/Qualifiers  
 1..422  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 3BOV"  
 /note="Vector: pCMV SPOR76; Site 1: NotI; Site 2: SalI;  
 Library made from pooled tissue from marrow, alveolar  
 macrophage, ovary, fetal semitendinosus muscle, and fetal  
 longissimus muscle."

ORIGIN  
 Query Match 34.5%; Score 178.2; DB 10; Length 422;  
 Best Local Similarity 72.3%; Pred. No. 3.7e-41;  
 Matches 245; Conservative 0; Mismatches 93; Indels 1; Gaps 1;

QY 9 GAACCTAAGGTCTCCTTTGACCTCCATG-GAATAGAAATATTTAAAGGAGAGAAATGTGA 67  
 Db |||||  
 84 GAAATCTAAGGGTGTCTTGAATCCACCATGAGAGAAAATATCTTAAAGGAGATGCTGTGA 143  
 QY 68 CTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAATGGTTCCACAATG 127  
 Db |||||  
 144 CTCTTACATGTTAGTACGATGGTTCTCTGAAGACCAGTCTCTCTGTGGNATCCCAATG 203  
 QY 128 GCAGCCTTTGAGAGAGACAATTCAGTTTGAATATGTAATGCCAAAATTTGAAGACA 187  
 Db |||||  
 204 GAACAGTTTTCACAAAGCAATATTCAGATGCCCAATTTGAAAGCAGCGATGAGGACA 263  
 QY 188 GTGGAGAATACAAATGTGAGACCAACAAAGTTAATGAGAGTGAACCTGTGTACCTGGAAG 247  
 Db |||||  
 264 GTGGGATACCATGCGGATCAAGGATTTGCCATCAGTGAACCCGTATACCTAAATG 323  
 QY 248 TCTTCAGTGACTGGTGTCTCTTCAGGCTCTGCTGAGGTGGTGTGATGAGGGCCAGCCCC 307  
 Db |||||  
 324 TCATCAGTGACTGGTGTGATCATTCAGGCTCTGCTGAGGTGATGATGAGGGTGAGTCCC 383  
 QY 308 TCTTCTCAGTGCATGCTGGTGGAGGACTGGGATGTGT 346  
 Db |||||  
 384 TCTTCTCAGTGCACACAGTTGGAGAAATCTGAATGTCT 422

RESULT 15  
 CB768694  
 LOCUS CB768694 403 bp mRNA linear EST 16-MAY-2003  
 DEFINITION AMGNNUC:SRPB2-00228-E10-A srpb2 (10220) Rattus norvegicus cDNA  
 clone srpb2-00228-e10 5', mRNA sequence.  
 ACCESSION CB768694  
 VERSION CB768694.1 GI:29857085  
 KEYWORDS EST.  
 ORGANISM Rattus norvegicus (Norway rat)  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.  
 1 (bases 1 to 403)  
 REFERENCE 1  
 AUTHORS Angen EST Program.  
 TITLE Angen Rat EST Program  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Dan Fitzpatrick  
 Angen, Inc  
 One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA  
 Tel: 805 447-4881  
 Plate: 00228 row: e column: 10.  
 FEATURES  
 source 1..403  
 /organism="Rattus norvegicus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10116"  
 /clone="srpb2-00228-e10"  
 /tissue\_type="prostate tissue"  
 /clone\_lib="srpb2 (10220)"  
 /note="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; rat  
 prostate normalized double selected poly(A+) mRNA size  
 fraction > 1 kb"

## ORIGIN

Query Match 34.0%; Score 175.6; DB 14; Length 403;  
 Best Local Similarity 69.9%; Pred. No. 2.1e-40;  
 Matches 235; Conservative 0; Mismatches 101; Indels 0; Gaps 0;  
 QY 181 GAAGCAGTGGAGAAATACAAATGTCAGCACCAACAAAGTTAATGAGAGTGAACCTGTGTAC 240  
 Db |||||  
 11 GAAGCAGTGGAAATATACATATGTGAGAAGCAAGGATTTTATAAGAGCAACCTGTGTAC 70  
 QY 241 CTGGAAGTCTTCAGTGAGTGGTGTCTTCAGGCTCTGCTGAGGTGGTGTGAGGGGC 300  
 Db |||||  
 71 TTGAACNTGATGANGAGTGGTGTCTGCTCCAAATCTTCTGCTGACGTGTGTAGACAAT 130

QY 301 CAGCCCTCTTCTCAGGTGCCATGGTTGAGGAACTGGGATGTGTACAAGGTGATCTAT 360  
 Db |||||  
 131 GGATCCTTTTGACATCAGATGCGGTAGCTGGAAAGAAATGAAAGTCCACAAGGTGATCTAC 190  
 QY 361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAACAACATCTCCATTACAAAT 420  
 Db |||||  
 191 TACAGGACGACATTTGCTTTCAAGTACTCTTATGACGCAACAACATCTCCATTAGAAG 250  
 QY 421 GCCACAGTTGAAGACAGTGGAACTTACTACTGTACGGGCAAAAGTGTGGCAGCTGGACTAT 480  
 Db |||||  
 251 GCCACATTTAATGACAGTGGCAGCTACCACCTGCACAGGCTATTTTGAACAAGTTGAATGT 310  
 QY 481 GAGTCTGAGCCCTTCAACATTTACTCTTAATAAAGCT 516  
 Db |||||  
 311 AAATCTGATAAATTCAGTATTGCTGTAGTAAAGAT 346

Search completed: October 10, 2004, 19:44:40  
 Job time : 1742.12 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:38 ; Search time 38.8904 Seconds  
(without alignments)  
1249.617 Million cell updates/sec

Title: US-10-763-400-13

Perfect score: 947

Sequence: 1 VPQKPKVSLNPNWIFKGE.....GKRWQLDYSEPLNITVIKA 172

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Geneseqp29Jan04:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp1990s:\*
- 4: Geneseqp2000s:\*
- 5: Geneseqp2001s:\*
- 6: Geneseqp2002s:\*
- 7: Geneseqp2003as:\*
- 8: Geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	947	100.0	172	2 AAY33185	Aay33185 Human SPC
2	947	100.0	172	3 AAY94211	Aay94211 Human PhP
3	947	100.0	172	3 AAB31587	Aab31587 A Fc epsi
4	947	100.0	176	3 AAY94210	Aay94210 Human PhP
5	947	100.0	176	4 AAG65597	Aag65597 Amino aci
6	947	100.0	182	3 AAY96234	Aay96234 Recombina
7	947	100.0	183	3 AAY96232	Aay96232 Recombina
8	947	100.0	197	2 AAR45778	Aar45778 Human diH
9	947	100.0	197	4 AAB31586	Aab31586 A Fc epsi
10	947	100.0	232	4 AAB31585	Aab31585 Amino aci
11	947	100.0	235	2 AAR26064	Aar26064 Human FcE
12	947	100.0	257	1 AAR90385	Aap90385 Alpha sub
13	947	100.0	257	2 AAR05025	Aar05025 Alpha sub
14	947	100.0	257	2 AAR14772	Aar14772 Human Fc(
15	947	100.0	257	2 AAR42336	Aar42336 Human Fce
16	947	100.0	257	2 AAW24066	Aaw24066 Alpha sub
17	947	100.0	257	2 AAW61190	Aaw61190 The alpha
18	947	100.0	257	2 AAW48094	Aaw48094 Human IGE
19	947	100.0	257	4 AAB74667	Aab74667 Human imm
20	947	100.0	257	4 AAB31584	Aab31584 Amino aci
21	947	100.0	257	5 AAG32801	Aag32801 Human IGE
22	947	100.0	257	6 ABO01301	Abc01301 Human pro
23	947	100.0	257	7 ABE85536	Abd85536 Human imm
24	947	100.0	257	7 ADD48674	Add48674 Human Pro
25	947	100.0	260	3 AAY96230	Aay96230 Human Fc

26	947	100.0	635	4 AAB31594	Aab31594 Fc epsilo
27	947	100.0	660	4 AAB31593	Aab31593 Fc epsilo
28	947	100.0	731	4 AAB31591	Aab31591 Amino aci
29	947	100.0	756	4 AAB31590	Aab31590 Amino aci
30	947	100.0	978	2 AAW48096	Aaw48096 Human ser
31	947	100.0	978	5 AAG32803	Aag32803 Human IGE
32	931	98.3	193	2 AAR89281	Aar89281 IGE high
33	922	97.4	176	4 AAG65598	Aag65598 Amino aci
34	851	89.9	247	2 AAR30483	Aar30483 Human hig
35	775	81.8	281	2 AAR13867	Aar13867 Hybrid FC
36	714.5	75.4	218	6 ABO01302	Abc01302 Human pro
37	679	71.7	281	2 AAR13870	Aar13870 Hybrid FC
38	639	67.5	281	2 AAR13872	Aar13872 Fc(gamma)
39	606	64.0	281	2 AAR13869	Aar13869 Hybrid FC
40	570	60.2	201	2 AAY27061	Aay27061 Recombina
41	570	60.2	236	2 AAY27060	Aay27060 Equine FC
42	570	60.2	255	2 AAY27058	Aay27058 Equine FC
43	564	59.6	190	5 AAE18631	Aae18631 Equine hi
44	522	55.1	199	2 AAW81111	Aaw81111 Canine FC
45	516	54.5	197	2 AAW81115	Aaw81115 Canine FC

#### ALIGNMENTS

##### RESULT 1

AAY33185  
ID AAY33185 standard; protein; 172 AA.

XX AAY33185;

XX 15-NOV-1999 (first entry)

XX Human sFC-epsilonRI protein fragment.

DE FC receptor; FC-gammaRIIa; human; FCR; model; three-dimension; 3-D;

KW atomic coordinate; bioactive compound design; computer-assisted;

KW drug design; therapy; inhibitor; FC-gammaR; FC-epsilonR; IGG; IGE;

KW tissue damage; hypersensitivity; inflammatory cell recruitment;

KW inflammatory modulator; FC-gammaRIa; immune function regulation;

XX anti-inflammatory; immunoprotective.

XX Homo sapiens.

XX WO9940117-Al.

XX 12-AUG-1999.

XX 04-FEB-1999; 99WO-IB000367.

XX 06-FEB-1998; 98US-0073972P.

PR 11-SEP-1998; 98US-0099994P.

XX (ILEX-) ILEXUS PTY LTD.

XX Hogarth PM, Powell MS, McKenzie IFC, Maxwell KF, Garrett TPJ;

PI Epa V, Baill JB, Matthews BR, McCarthy TD, Pietersz GA;

XX WPI; 1999-539978/45.

XX Three-dimensional structures and models of Fc receptors, useful in

PT computer-assisted drug design.

PS Claim 11; Page 318-319; 326pp; English.

XX This invention describes a novel model of an Fc receptor (FcR) protein  
CC representing a three-dimensional (3-D) structure that substantially  
CC conforms to the specified atomic coordinates. Computer model images of  
CC the FcR can be used to design bioactive chemical compounds, e.g.  
CC oligonucleotides, peptides, peptidomimetics and small organic molecules,  
CC by computer-assisted methods of drug design. Therapeutic compositions  
CC that inhibit the activity of FC-gammaR or FC-epsilonR can be used to  
CC reduce IgG- or IgE-mediated tissue damage, e.g. IgG- or IgE-mediated

CC hypersensitivity, recruitment of inflammatory cells or release of  
 CC inflammatory modulators. The therapeutic compositions can also be used to  
 CC treat disease in animals. The knowledge of the 3-D structure of Fc-gamma  
 CC R1a and models of other FcR provides a means for designing and producing  
 CC compounds that regulate immune function and inflammation in an animal,  
 CC including humans (i.e. structure based drug design). For example,  
 CC chemical compounds can be designed to block binding of immunoglobulin to  
 CC an Fc receptor protein using various computer programs and models. The  
 CC products of the invention have anti-inflammatory and immunoprotective  
 CC activity. This sequence represents the human sFc-epsilon1 protein  
 CC fragment described in the method of the invention  
 XX  
 XX Sequence 172 AA;

Query Match 100.0%; Score 947; DB 2; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-66;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNPFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60  
 Db 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNPFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60  
 QY 61 EDSGEYKCHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWNDVYKVIY 120  
 Db 61 EDSGEYKCHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWNDVYKVIY 120  
 QY 121 YKDGKALKYWYENHNISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172  
 Db 121 YKDGKALKYWYENHNISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172

RESULT 2  
 AAY94211  
 ID AAY94211 standard; protein; 172 AA.

XX AC AAY94211;

DT 01-AUG-2000 (first entry)

XX DE Human PhFcepsilon1RIalpha 1-172.

XX KW Protein co-ordinate data; PhFcepsilon1RIalpha 1-172; PCR;  
 KW Fcepsilon1RIalpha 1-172; antibody Fc receptor; allergy;  
 KW anaphylactic shock.

XX OS Homo sapiens.

XX FH Key  
 FT Region 7..10 Location/Qualifiers  
 FT /label= Beta\_sheet\_secondary\_structure  
 FT 14..15  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 19..25  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 37..40  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 44..45  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 53..55  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 63..68  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 76..82  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 89..92  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 96..97  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 101..107  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 118..121  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 125..127

FT /label= beta\_sheet\_secondary\_structure  
 FT 135..139  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 147..155  
 FT /label= beta\_sheet\_secondary\_structure  
 FT 158..170  
 FT /label= beta\_sheet\_secondary\_structure

XX WO200026246-A2.

XX 11-MAY-2000.

XX 05-NOV-1999; 99WO-US026203.

XX 05-NOV-1998; 98US-0107219P.

XX (HESK-) HESKA CORP.

XX (NOUN) UNIV NORTHWESTERN.

XX Jardtetzky TS, Garman SC, Kinet J;

XX WPI: 2000-365577/31.

XX N-PSDB; AAA27302.

XX Three-dimensional model comprising an extracellular domain of a human  
 PT high affinity Fc epsilon receptor alpha chain protein, useful for  
 PT identifying inhibitors and useful mutins.

XX Claim 6; Page 462; 463pp; English.

XX CC The present sequence is the human Fcepsilon1RIalpha 1-172 protein (also  
 CC known as PhFcepsilon1RIalpha 1-172). Along with either the Fcepsilon1RI  
 CC beta and/or gamma subunits, this protein is involved in mast cell  
 CC activation and the triggering of allergic reactions and anaphylactic  
 CC shock. The protein can be used to identify useful mutins and inhibitors,  
 CC which can then be used in the detection of (susceptibility to) allergies  
 CC and in protecting animals from these allergies

XX Sequence 172 AA;

Query Match 100.0%; Score 947; DB 3; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-66;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNPFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60

Db 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNPFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60

QY 61 EDSGEYKCHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWNDVYKVIY 120

Db 61 EDSGEYKCHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWNDVYKVIY 120

QY 121 YKDGKALKYWYENHNISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172

Db 121 YKDGKALKYWYENHNISITNATVEDSGTYCTGKQWQLDYSEPLNITVIKA 172

RESULT 3

AAB31587

ID AAB31587 standard; protein; 172 AA.

XX AC AAB31587;

XX 30-APR-2001 (first entry)

XX DE A Fc epsilon receptor alpha-chain secretable protein.

XX KW Fc epsilon receptor; Fcepsilon1RI; immunoglobulin E; IgE; atopic disease;  
 KW luminescence inducing protein; allergy; hyper IgE syndrome;  
 XX internal parasite infection; B cell neoplasia.

XX OS Homo sapiens.

XX

PN WO200104310-A1.  
XX 18-JAN-2001.  
XX 13-JUL-2000; 2000WO-US019070.  
XX 13-JUL-1999; 99US-0143612P.  
PR 02-MAR-2000; 2000US-0186412P.  
XX (HESK-) HESKA CORP.  
XX (PROM-) PROMEGA CORP.  
PA Weber ER, Wood KV, Hall MP;  
XX WPI; 2001-103082/11.  
DR N-PSDB; AAF24917.  
XX A fusion protein, comprising an Fc epsilon receptor domain and a  
PT luminescence inducing protein domain that induces a LP substrate to emit  
PT light when contacted with the LP domain, useful for detecting  
PT immunoglobulin (Ig) E.  
XX  
XX Claim 16; Page 67; 105pp; English.  
XX  
XX The present sequence represents a secretable form of a human Fc epsilon  
CC receptor (FcepsilonR) alpha-chain. The FcepsilonR protein binds to  
CC immunoglobulin (Ig) E. The FcepsilonR domain is used to produce a fusion  
CC protein, which also comprises a luminescence inducing protein domain that  
CC induces a substrate to emit light when contacted with the luminescence  
CC inducing protein domain. The fusion protein may be used to detect IgE. It  
CC may also be used to identify a compound capable of inhibiting FcepsilonR  
CC protein activity. IgE antibody production is indicative of diseases such  
CC as allergies, atopic disease, hyper IgE syndrome, internal parasite  
CC infections and B cell neoplasia. Detection of IgE production in an animal  
CC following therapy is indicative of the efficacy of the treatment, for  
CC example when using treatments intended to disrupt IgE production.  
XX  
XX Sequence 172 AA;  
XX  
XX Query Match 100.0%; Score 947; DB 4; Length 172;  
XX Best Local Similarity 100.0%; Pred. No. 4.1e-66;  
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VPQPKVSLNPPNRRIFKGENVLTLCNGNNFFEVSTKWFHNGSLSEETNSSLNIVNAKF 60  
DB 1 VPQPKVSLNPPNRRIFKGENVLTLCNGNNFFEVSTKWFHNGSLSEETNSSLNIVNAKF 60  
QY 61 EDGGEYKCOHQVNESPVYLEVPSDWLLILOASAEVVMGQPLFLRCHGRNWDVVKVIY 120  
DB 61 EDGGEYKCOHQVNESPVYLEVPSDWLLILOASAEVVMGQPLFLRCHGRNWDVVKVIY 120  
QY 121 YKDGKALKYWEHNENISITNATVEDSGTYCTGKVQWLDYSEPLNITVIKA 172  
DB 121 YKDGKALKYWEHNENISITNATVEDSGTYCTGKVQWLDYSEPLNITVIKA 172  
RESULT 4  
AAAY94210  
ID AAAY94210 standard; protein; 176 AA.  
XX  
XX AAAY94210;  
XX  
XX 01-AUG-2000 (first entry)  
XX Human PhFcepsilonRIalpha 1-176.  
XX Protein co-ordinate data; PhFcepsilonRIalpha 1-176; FcR;  
XX FcepsilonRIalpha 1-176; antibody Fc receptor; allergy;  
XX anaphylactic shock.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers

FT Region  
FT /label= Beta\_sheet\_secondary\_structure  
FT 14..15  
FT /label= beta\_sheet\_secondary\_structure  
FT 19..25  
FT /label= beta\_sheet\_secondary\_structure  
FT 37..40  
FT /label= beta\_sheet\_secondary\_structure  
FT 44..45  
FT /label= beta\_sheet\_secondary\_structure  
FT 53..55  
FT /label= beta\_sheet\_secondary\_structure  
FT 63..68  
FT /label= beta\_sheet\_secondary\_structure  
FT 76..82  
FT /label= beta\_sheet\_secondary\_structure  
FT 89..92  
FT /label= beta\_sheet\_secondary\_structure  
FT 96..97  
FT /label= beta\_sheet\_secondary\_structure  
FT 101..107  
FT /label= beta\_sheet\_secondary\_structure  
FT 118..121  
FT /label= beta\_sheet\_secondary\_structure  
FT 125..127  
FT /label= beta\_sheet\_secondary\_structure  
FT 135..139  
FT /label= beta\_sheet\_secondary\_structure  
FT 147..155  
FT /label= beta\_sheet\_secondary\_structure  
FT 158..170  
FT /label= beta\_sheet\_secondary\_structure  
PN WO200026246-A2.  
XX  
XX 11-MAY-2000.  
XX  
XX 05-NOV-1999; 99WO-US026203.  
XX  
XX 05-NOV-1998; 98US-0107219P.  
XX (HESK-) HESKA CORP.  
XX (NOUN) UNIV NORTHWESTERN.  
XX  
XX Jardtetzky TS, Garman SC, Kinet J;  
XX WPI; 2000-365577/31.  
XX N-PSDB; AAA27301.  
XX  
XX Three-dimensional model comprising an extracellular domain of a human  
PT high affinity Fc epsilon receptor alpha chain protein, useful for  
PT identifying inhibitors and useful muteins.  
XX  
XX Claim 6; Page 460; 463pp; English.  
XX  
XX The present sequence is the human FcepsilonRIalpha 1-176 protein (also  
CC known as PhFcepsilonRIalpha 1-176). Along with either the FcepsilonRI  
CC beta and/or gamma subunits, this protein is involved in mast cell  
CC activation and the triggering of allergic reactions and anaphylactic  
CC shock. The protein can be used to identify useful muteins and inhibitors,  
CC which can then be used in the detection of (susceptibility to) allergies  
CC and in protecting animals from these allergies  
XX  
XX Sequence 176 AA;  
XX  
XX Query Match 100.0%; Score 947; DB 3; Length 176;  
XX Best Local Similarity 100.0%; Pred. No. 4.2e-66;  
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VPQPKVSLNPPNRRIFKGENVLTLCNGNNFFEVSTKWFHNGSLSEETNSSLNIVNAKF 60  
DB 1 VPQPKVSLNPPNRRIFKGENVLTLCNGNNFFEVSTKWFHNGSLSEETNSSLNIVNAKF 60

QY 61 EDSEYKCOHQWNESEPVYLEVFSDDLLOQSAEVMVEGQPLFLRCHGRNWDVYKVIY 120  
 Db 61 EDSEYKCOHQWNESEPVYLEVFSDDLLOQSAEVMVEGQPLFLRCHGRNWDVYKVIY 120  
 QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYESEPLNITVIKA 172  
 Db 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYESEPLNITVIKA 172

## RESULT 5

AA65597  
 ID AAG65597 standard; protein; 176 AA.

XX AC AAG65597;

XX DT 07-JAN-2002 (first entry)

XX DE Amino acid sequence of PhCepsilonRIalpha1-176 protein.

XX KW Antibody receptor protein; FcpepsilonRIalpha protein; immunoglobulin; IgE;  
 KW mutein; allergy; protein co-ordinate.

XX OS Homo sapiens.

XX PN WO200169253-A2.

XX PD 20-SEP-2001.

XX PF 14-MAR-2001; 2001WO-US008588.

XX PR 15-MAR-2000; 2000US-0189853P.

XX PA (HESK-) HESKA CORP.

XX PA (NOUN) UNIV NORTHWESTERN.

XX PI Jardtzy TS, Garman SC, Wurzburg BA, Kinet J;

XX DR WPI; 2001-611403/70.

XX DR N-PSDB; AAH47768.

XX PT Three dimensional models of complexes between antibody receptor proteins  
 PT and antibodies used to identify modulators of antibody/receptor binding.

XX PS Claim 11; Page 209-210; 213pp; English.

XX CC The invention relates to three dimensional models of complexes between  
 CC antibody receptor proteins, especially FcpepsilonRIalpha proteins, and  
 CC antibodies, especially Fc-Cepsilon3/Cepsilon4 regions of immunoglobulin  
 CC (Ig) E antibodies. The models are used to identify an inhibitor of the  
 CC selective binding between a FcpepsilonRIalpha protein and an IgE antibody.  
 CC The model identifies crystal contacts between a FcpepsilonRIalpha protein  
 CC and an Fc-Cepsilon3/Cepsilon4 region of an IgE antibody. A mutein that  
 CC binds to an Fc domain of an antibody (the mutein has improved function  
 CC improved stability, increased affinity for an Fc domain of an antibody,  
 CC altered substrate specificity, increased affinity for an Fc domain of an  
 CC antibody, altered substrate specificity, and increased solubility)  
 CC compared to a protein comprising a defined amino acid sequence given in  
 CC the specification) is used: to protect an animal from an allergy; detect  
 CC an allergy in an animal; and to enhance the performance of an IgE binding  
 CC assay. The present sequence represents the amino acid sequence of a  
 CC PhCepsilonRIalpha1-176 protein

XX SQ Sequence 176 AA;

Query Match 100.0%; Score 947; DB 4; Length 176;

Best Local Similarity 100.0%; Pred. No. 4.28-56;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKFGENVTLTCGNPNFFVSSTKWFHNGSLSEETNSSLINIVNAKF 60

Db 1 VPQPKVSLNPPNRIKFGENVTLTCGNPNFFVSSTKWFHNGSLSEETNSSLINIVNAKF 60

QY 61 EDSEYKCOHQWNESEPVYLEVFSDDLLOQSAEVMVEGQPLFLRCHGRNWDVYKVIY 120

Db 61 EDSEYKCOHQWNESEPVYLEVFSDDLLOQSAEVMVEGQPLFLRCHGRNWDVYKVIY 120  
 QY 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYESEPLNITVIKA 172  
 Db 121 YKDGALKYWNHNISITNATVEDSGTYCTGKWQLDYESEPLNITVIKA 172

## RESULT 6

AA96234

ID AAY96234 standard; protein; 182 AA.

XX AC AAY96234;

XX DT 11-SEP-2000 (first entry)

XX DE Recombinant human Fc receptor, FcgammaRIIb, # 4.

XX KW Human; Fc receptor; FcgammaRIIb; immunoglobulin; infection;  
 KW immune response; HIV; IgG; immunosuppressive; antirheumatic;  
 KW antiinflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;  
 KW systemic lupus erythematosus; tumour.

XX OS Homo sapiens.

XX PN EP1006183-A1.

XX PD 07-JUN-2000.

XX PF 03-DEC-1998; 98EP-00122969.

XX PR 03-DEC-1998; 98EP-00122969.

XX PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX WPI; 2000-367968/32.

XX DR N-PSDB; AA27472.

XX PT Novel Fc receptor lacking transmembrane domains, a signal peptide, and  
 PT glycosylation, useful for diagnosing and treating immune disorders and  
 PT cancer.

XX PS Claim 5; Page 15; 60pp; English.

XX CC The present sequence is the recombinant human Fc receptor, FcgammaRIIb.  
 CC Fc receptors play an important role in defending the body against  
 CC infections. First, pathogens are opsonised by serum immunoglobulins. The  
 CC resulting complex then binds to cells expressing Fc receptors. Upon Fc  
 CC receptor activation, immune effector pathways are activated, leading to  
 CC immune response. The present recombinant Fc receptor consists only of the  
 CC extracellular portion of the wildtype receptor and are not glycosylated  
 CC i.e. they do not have transmembrane domains or signal peptides. The  
 CC recombinant proteins may be used in immunoassays to determine the immune  
 CC status of patients with chronic diseases of the immune system, e.g. AIDS,  
 CC systemic lupus erythematosus (SLE), multiple myeloma (MM), or rheumatoid  
 CC arthritis. In addition, pharmaceutical compositions containing  
 CC recombinant proteins may be used to treat or prevent autoimmune diseases,  
 CC allergies or tumours, especially AIDS, rheumatoid arthritis or MM. Note:  
 CC the present sequence differs from that shown in the sequence listing of  
 CC the specification (AAY96232). The AAY96232 sequence has an additional Met  
 CC at the N-terminal

XX SQ Sequence 182 AA;

Query Match 100.0%; Score 947; DB 3; Length 182;

Best Local Similarity 100.0%; Pred. No. 4.4e-66;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKFGENVTLTCGNPNFFVSSTKWFHNGSLSEETNSSLINIVNAKF 60

Db 2 VPQPKVSLNPPNRIKFGENVTLTCGNPNFFVSSTKWFHNGSLSEETNSSLINIVNAKF 61

QY 61 EDSEYKCOHQWNESEPVYLEVFSDDLLOQSAEVMVEGQPLFLRCHGRNWDVYKVIY 120

Db 62 EDSEYKQHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 121  
QY 121 YKDGALKYWEHNHNSITNATVEDSGTYCTGKWQWLDYSEPLNITVIKA 172  
Db 122 YKDGALKYWEHNHNSITNATVEDSGTYCTGKWQWLDYSEPLNITVIKA 173

RESULT 7  
AAY96232  
ID AAY96232 standard; protein; 183 AA.  
XX  
AC AAY96232;  
XX  
DT 11-SEP-2000 (first entry)  
XX  
DE Recombinant human Fc receptor, Fc gammaRIIb, # 2.  
XX Human; Fc receptor; Fc gammaRIIb; immunoglobulin; infection;  
KW immune response; HIV; IGG; immunosuppressive; antirheumatic;  
KW antinflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;  
KW systemic lupus erythematosus; tumour.  
XX  
OS Homo sapiens.  
XX  
PN EP1006183-A1.  
XX  
PD 07-JUN-2000.  
XX  
PF 03-DEC-1998; 98EP-00122969.  
XX  
PR 03-DEC-1998; 98EP-00122969.  
XX  
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
XX  
DR WPI; 2000-367968/32.  
DR N-PSDB; AAA27472.  
XX  
PT Novel Fc receptor lacking transmembrane domains, a signal peptide, and  
glycosylation, useful for diagnosing and treating immune disorders and  
cancer.  
XX  
PS Claim 5; Page 45-46; 60pp; English.

XX The present sequence is the recombinant human Fc receptor, Fc gammaRIIb.  
CC Fc receptors play an important role in defending the body against  
CC infections. First, pathogens are opsonised by serum immunoglobulins. The  
CC resulting complex then binds to cells expressing Fc receptors. Upon Fc  
CC receptor activation, immune effector pathways are activated, leading to  
CC immune response. The present recombinant Fc receptor consists only of the  
CC extracellular portion of the wildtype receptor and are not glycosylated  
CC i.e. they do not have transmembrane domains or signal peptides. The  
CC recombinant proteins may be used in immunoassays to determine the immune  
CC status of patients with chronic diseases of the immune system, e.g. AIDS,  
CC systemic lupus erythematosus (SLE), multiple myeloma (MM), or rheumatoid  
CC arthritis. In addition, pharmaceutical compositions containing  
CC recombinant proteins may be used to treat or prevent autoimmune diseases,  
CC allergies or tumours, especially AIDS, rheumatoid arthritis or MM. Note:  
CC the present sequence differs from that shown on page 15 of the  
CC specification (AAY96234). The present sequence has an additional Met at  
CC the N-terminal  
XX  
SQ Sequence 183 AA;

Query Match 100.0%; Score 947; DB 3; Length 183;  
Best Local Similarity 100.0%; Pred. No. 4.4e-66;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VPQPKVSLNPPNRRIFKGNVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60  
Db 3 VPQPKVSLNPPNRRIFKGNVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 62  
QY 61 EDSEYKQHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120

Db 63 EDSEYKQHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 122  
QY 121 YKDGALKYWEHNHNSITNATVEDSGTYCTGKWQWLDYSEPLNITVIKA 172  
Db 123 YKDGALKYWEHNHNSITNATVEDSGTYCTGKWQWLDYSEPLNITVIKA 174

RESULT 8  
AAR45778  
ID AAR45778 standard; protein; 197 AA.  
XX  
AC AAR45778;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-SEP-1994 (first entry)  
XX  
DE Human dihydrofolate reductase (DHFR).  
XX Dihydrofolate reductase; DHFR; marker; transformation.  
KW  
OS Homo sapiens.  
XX  
PN WO9403598-A1.  
XX  
PD 17-FEB-1994.  
XX  
PF 03-AUG-1993; 93WO-JP001085.  
XX  
PR 04-AUG-1992; 92JP-00229227.  
PR 10-AUG-1992; 92JP-00213002.  
PR 08-OCT-1992; 92JP-00270513.  
PR 08-OCT-1992; 92JP-00270514.  
PR 08-OCT-1992; 92JP-00270515.  
XX  
PA (GREC ) GREEN CROSS CORP.  
XX  
PI Ra C, Naito K, Hiram M, Okumura K;  
DR WPI; 1994-065687/08.  
DR N-PSDB; AAQ55969.  
XX  
PT Antiallergic peptide derived from high-affinity immunoglobulin E receptor  
PT - binds to human immunoglobulin E to block allergic reactions at source.  
XX  
PS Disclosure; Page 24-25; 37pp; Japanese.  
XX  
CC The dihydrofolate reductase (DHFR) gene was used in the construction of a  
CC vector as a selectable marker. The resulting vector was used to transform  
CC DHFR-deficient CHO cells. (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 197 AA;

Query Match 100.0%; Score 947; DB 2; Length 197;  
Best Local Similarity 100.0%; Pred. No. 4.8e-66;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VPQPKVSLNPPNRRIFKGNVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60  
Db 26 VPQPKVSLNPPNRRIFKGNVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 85  
QY 61 EDSEYKQHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
Db 86 EDSEYKQHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145

Query Match 100.0%; Score 947; DB 3; Length 183;  
Best Local Similarity 100.0%; Pred. No. 4.4e-66;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VPQPKVSLNPPNRRIFKGNVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 60  
Db 3 VPQPKVSLNPPNRRIFKGNVTLTCNGNFFVSSSTKWFHNGSLSEETNSSLNIVNAKF 62  
QY 61 EDSEYKQHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120

RESULT 9  
AAB31586  
ID AAB31586 standard; protein; 197 AA.

```

XX AAB31586;
AC
XX 30-APR-2001 (first entry)
DT
XX
DE A Fc epsilon receptor alpha-chain extracellular domain.
XX
XX Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia.
XX
OS Homo sapiens.
XX
XX WO200104310-A1.
PN
XX
XX 18-JAN-2001.
PD
XX
XX 13-JUL-2000; 2000WO-US019070.
PF
XX
XX 13-JUL-1999; 99US-0143612P.
PR
XX 02-MAR-2000; 2000US-0186412P.
PR
XX
XX (HESK-) HESKA CORP.
PA
XX (PROM-) PROMEGA CORP.
PA
XX
XX Weber ER, Wood KV, Hall MP;
PI
XX
XX WPI; 2001-103082/11.
DR
XX N-PSDB; AAF24915.
DR
XX
XX A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
PT immunoglobulin (Ig) E.
XX
XX Claim 16; Page 65; 105pp; English.
XX
XX The present sequence represents the extracellular domain of a human Fc
CC epsilon receptor (FcepsilonR) alpha-chain. The FcepsilonR protein binds
CC to immunoglobulin (Ig) E. The FcepsilonR domain is used to produce a
CC fusion protein, which also comprises a luminescence inducing protein
CC domain that induces a substrate to emit light when contacted with the
CC luminescence inducing protein domain. The fusion protein may be used to
CC detect IgE. It may also be used to identify a compound capable of
CC inhibiting FcepsilonR protein activity. IgE antibody production is
CC indicative of diseases such as allergies, atopic disease, hyper IgE
CC syndrome, internal parasite infections and B cell neoplasia. Detection of
CC IgE production in an animal following therapy is indicative of the
CC efficacy of the treatment, for example when using treatments intended to
CC disrupt IgE production
XX
XX Sequence 197 AA;
Query Match 100.0%; Score 947; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.8e-66;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQKPKVSLNPPWNRIFKGENVTITCGNNPFVSVSTKWFHNGSLSEETNSSLINIVNAKF 60
DB 26 VPQKPKVSLNPPWNRIFKGENVTITCGNNPFVSVSTKWFHNGSLSEETNSSLINIVNAKF 65
QY 61 EDSEYKCKQHQVNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
DB 86 EDSEYKCKQHQVNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 145
QY 121 YKGEALKYWEHNHNSITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
DB 146 YKGEALKYWEHNHNSITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197
RESULT 10
AAB31585
ID AAB31585 standard; protein; 232 AA.

```

```

XX AAB31585;
AC
XX 30-APR-2001 (first entry)
DT
XX
DE Amino acid sequence of Fc epsilon receptor alpha-chain mature protein.
XX
XX Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia.
XX
OS Homo sapiens.
XX
XX WO200104310-A1.
PN
XX
XX 18-JAN-2001.
PD
XX
XX 13-JUL-2000; 2000WO-US019070.
PF
XX
XX 13-JUL-1999; 99US-0143612P.
PR
XX 02-MAR-2000; 2000US-0186412P.
PR
XX
XX (HESK-) HESKA CORP.
PA
XX (PROM-) PROMEGA CORP.
PA
XX
XX Weber ER, Wood KV, Hall MP;
PI
XX
XX WPI; 2001-103082/11.
DR
XX N-PSDB; AAF24913.
DR
XX
XX A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
PT immunoglobulin (Ig) E.
XX
XX Claim 16; Page 62-63; 105pp; English.
XX
XX The present sequence represents a human Fc epsilon receptor (FcepsilonR)
CC alpha-chain mature protein, that binds to immunoglobulin (Ig) E. The
CC FcepsilonR domain is used to produce a fusion protein, which also
CC comprises a luminescence inducing protein domain that induces a substrate
CC to emit light when contacted with the luminescence inducing protein
CC domain. The fusion protein may be used to detect IgE. It may also be used
CC to identify a compound capable of inhibiting FcepsilonR protein activity.
CC IgE antibody production is indicative of diseases such as allergies,
CC atopic disease, hyper IgE syndrome, internal parasite infections and B
CC cell neoplasia. Detection of IgE production in an animal following
CC therapy is indicative of the efficacy of the treatment, for example when
CC using treatments intended to disrupt IgE production
XX
XX Sequence 232 AA;
Query Match 100.0%; Score 947; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 5.8e-66;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQKPKVSLNPPWNRIFKGENVTITCGNNPFVSVSTKWFHNGSLSEETNSSLINIVNAKF 60
DB 1 VPQKPKVSLNPPWNRIFKGENVTITCGNNPFVSVSTKWFHNGSLSEETNSSLINIVNAKF 60
QY 61 EDSEYKCKQHQVNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
DB 61 EDSEYKCKQHQVNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120
QY 121 YKGEALKYWEHNHNSITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
DB 121 YKGEALKYWEHNHNSITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
RESULT 11
AAR26064
ID AAR26064 standard; protein; 235 AA.
XX

```



```

AC AAR26064;
XX
XX 25-MAR-2003 (revised)
DT
DT 02-FEB-1993 (first entry)
XX
XX Human FcERI alpha-subunit and IL-2 hybrid protein.
XX
XX High affinity Fc immunoglobulin E receptor; IGE; antibody; interleukin-2;
KW histamine release; allergy.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 26..201
FT /label= human FcERI alpha-subunit
FT /note= "epitope recognised by new MAB"
XX
XX EP499112-A1.
XX
XX 19-AUG-1992.
PD
XX
XX 03-FEB-1992; 92EP-00101732.
PF
XX
XX 11-FEB-1991; 91US-00653936.
PR
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA
XX Chizzonite RA, Hakimi J, Kochan JP;
XX
XX WPI; 1992-277871/34.
DR
XX
XX Monoclonal antibodies bind to alpha sub-unit of Fc IGE receptor - for
PT treatment and prevention of IGE induced allergic diseases, also for
PT measuring alpha sub-unit and IGE levels in biological fluids.
XX
XX Disclosure; Page 8; 30pp; English.
XX
XX This is a preferred protein for use in generating the monoclonal
CC antibodies of the invention. The protein comprises an epitope of the
CC human FcERI alpha-subunit to which the cytoplasmic and transmembrane
CC regions of the IL-2 receptor have been fused. (Cytoplasmic and
CC transmembrane regions from receptors other IL- 2 receptor can be also
CC used). The specification includes a nucleotide coding sequence which is a
CC preferred fusion gene (see AAR2767); the polypeptide which is decoded
CC from that fusion gene differs from the amino acid sequence AAR26064 as
CC follows: amino acids 5-7 are Arg-Ile-Leu (not Met-Glu-Ser), amino acid
CC 209 is Cys (not Lys), amino acid 229 is Ser (not Arg), Arg233 is absent
CC and an additional C-terminal amino acid (Phe) is present. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX SQ Sequence 235 AA;
Query Match 100.0%; Score 947; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 5.9e-66;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60
DB 26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 85
QY 61 EDSGEYKCOHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 86 EDSGEYKCOHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGEALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
DB 146 YKDGEALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197
RESULT 12
AAP90385
ID AAP90385 standard; protein; 257 AA.
XX

```

```

AC AAP90385;
XX
XX 24-OCT-2003 (revised)
DT
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
XX Alpha subunit of human mast cell IGE surface receptor.
XX
XX Immunoglobulin E receptor alpha subunit; allergies;
KW non-peptide drug design; human.
XX
XX Homo sapiens; (Human); mast cell line.
OS
XX KU812.
XX
XX WO8905352-A.
FN
XX 15-JUN-1989.
PD
XX 29-NOV-1988; 88WO-US004255.
PF
XX 01-DEC-1987; 87US-00127214.
PR
XX (HARD ) HARVARD COLLEGE.
PA (USSH ) NAT INST OF HEALTH.
XX
XX Leder P, Benfey P;
XX
XX WPI; 1989-192698/26.
DR N-PSDB; AAN90126.
XX
XX CDNA encoding IGE receptor alpha-sub-unit - used to treat allergies.
PT
XX Disclosure; Fig 4; 17pp; English.
XX
XX Immunoglobulin E receptor alpha subunit of human mast cell IGE surface
CC receptor (see corresp. AAN90126). Used to produce antibodies which can
CC diagnose IGE receptor levels, measure and treat allergies, and design non
CC -peptide drugs. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
CC 24-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 257 AA;
Query Match 100.0%; Score 947; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.5e-66;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60
DB 26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 85
QY 61 EDSGEYKCOHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120
DB 86 EDSGEYKCOHQOVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 145
QY 121 YKDGEALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
DB 146 YKDGEALKYWEYENHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197
RESULT 13
AAR05025
ID AAR05025 standard; protein; 257 AA.
XX
XX AAR05025;
AC
XX 02-OCT-1990 (first entry)
DT
XX Alpha subunit of human high affinity IGE receptor.
DE
XX high affinity IGE receptor; alpha subunit of IGE receptor; human;
KW allergic response; ss.
XX
XX Synthetic.
OS

```

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XX WO9004640-A.
XX PN
XX 03-MAY-1990.
XX PD
XX 18-OCT-1988; 88US-00259065.
XX PF
XX 18-OCT-1988; 88US-00259065.
XX PR
XX (USDC ) US SEC OF COMMERCE.
XX PA
XX Kinet JP, Metzger H;
XX PI
XX WPI; 1990-164023/21.
XX DR
XX N-PSDB; AAQ04644.
XX PT
XX DNA sequences for sub-unit peptide(s) of high affinity IgE receptor - and
XX derived polypeptides, for therapy and diagnosis of allergies, and studies
XX of IgE receptor interaction.
XX PS
XX Disclosure; Page ?; -pp; English.
XX CC
XX The high affinity receptor is a tetrameric complex consisting of 2 gamma
XX subunits and one each of subunits alpha and beta. It is expressed on mast
XX cells and is involved in the allergic response. COS-7 cells cotransfected
XX with cDNA for all 3 intact subunit types (derived from rat basophilic
XX leukaemia cells) express receptor on their surfaces. Detailed study of
XX the receptors is now possible. See also AAQ04643 and AAQ04645-6
XX SQ
XX Sequence 257 AA;
XX
XX Query Match 100.0%; Score 947; DB 2; Length 257;
XX Best Local Similarity 100.0%; Pred. No. 6.5e-66;
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VPQPKVSLNPPWNRIFKGENVTITCNGNPFVSVSTKWFHNGSLSEBTSSSLNIVNAKF 60
XX DB 26 VPQPKVSLNPPWNRIFKGENVTITCNGNPFVSVSTKWFHNGSLSEBTSSSLNIVNAKF 85
XX
XX QY 61 EDGSEYKQHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVVKVIY 120
XX DB 86 EDGSEYKQHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVVKVIY 145
XX
XX QY 121 YKDGKALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
XX DB 146 YKDGKALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197
XX
XX RESULT 14
XX AAR14772
XX ID AAR14772 standard; protein; 257 AA.
XX AC AAR14772;
XX XX
XX 25-MAR-2003 (revised)
XX DT 17-DEC-2001 (revised)
XX DT 03-FEB-1992 (first entry)
XX DE Human Fc(epsilon)RI alpha subunit.
XX XX
XX Immunoglobulin; receptor; high affinity receptor.
XX KW
XX Homo sapiens.
XX OS
XX
XX Key Location/Qualifiers
XX Peptide 1..25
XX FT /label= signal
XX FT 26..257
XX FT /label= alpha_subunit
XX FT 80..104
XX FT /label= homologous_domain
XX FT /notes= "homologous to residues 163-190"
XX FT 163..190

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FT FT /label= homologous_domain
FT FT /notes= "homologous to residues 80-104"
FT FT 205..224
FT FT /label= transmembrane
FT FT 225..257
FT FT /label= cytoplasmic
XX
XX USN7626704-N.
XX PN
XX 15-OCT-1991.
XX PD
XX 14-DEC-1990; 90US-00626704.
XX PF
XX 14-DEC-1990; 90US-00626704.
XX PR
XX (USSH ) NAT INST OF HEALTH.
XX PA
XX Kinet JP, Metzger H;
XX PI
XX WPI; 1991-346755/47.
XX DR
XX N-PSDB; AAQ14736.
XX DR
XX DNA coding alpha, beta and gamma-units of ige high affinity receptor -
XX used to prepare recombinant polypeptide(s) for treating allergy, drug
XX screening or monitoring IGE level.
XX PS
XX Disclosure; Fig 1; 58pp; English.
XX XX
XX A lambda gtl1 library was prepared from poly-A RNA isolated from KUB12
XX cells. Screening was by a cDNA fragment from the rat Fc(epsilon)RI alpha
XX cDNA corresponding to nucleotides 119-781. Positive clones were subcloned
XX and sequenced. This amino acid sequence was deduced from the cDNA clone.
XX (Note: Revised entry submitted to correct the patent number format of US
XX Government-owned NTIS applications to prevent clashes with ongoing US
XX granted patent numbers. For further information please visit the Derwent
XX web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-
XX MAR-2003 to correct PF field.)
XX SQ
XX Sequence 257 AA;
XX
XX Query Match 100.0%; Score 947; DB 2; Length 257;
XX Best Local Similarity 100.0%; Pred. No. 6.5e-66;
XX Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VPQPKVSLNPPWNRIFKGENVTITCNGNPFVSVSTKWFHNGSLSEBTSSSLNIVNAKF 60
XX DB 26 VPQPKVSLNPPWNRIFKGENVTITCNGNPFVSVSTKWFHNGSLSEBTSSSLNIVNAKF 85
XX
XX QY 61 EDGSEYKQHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVVKVIY 120
XX DB 86 EDGSEYKQHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVVKVIY 145
XX
XX QY 121 YKDGKALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172
XX DB 146 YKDGKALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197
XX
XX RESULT 15
XX AAR42336
XX ID AAR42336 standard; protein; 257 AA.
XX XX
XX AAR42336;
XX AC
XX 25-MAR-2003 (revised)
XX DT 21-JUN-1994 (first entry)
XX DE Human FcεRI alpha.
XX XX
XX IgE; immunoglobulin E receptor; beta subunit; basophils; allergy;
XX aggregation; signal transduction; diagnosis; antagonist.
XX KW
XX Homo sapiens.
XX OS
XX

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Search completed: October 6, 2004, 09:03:08  
Job time : 39.8904 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:40 ; Search time 11.2261 Seconds  
(without alignments)  
790.984 Million cell updates/sec

Title: US-10-763-400-13

Perfect score: 947

Sequence: 1 VPQPKVSLNPPNRIKGE.....GKWLQDYSEPLNITVIKA 172

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	947	100.0	172	2	US-08-756-387B-13
2	947	100.0	172	4	US-09-285-873-13
3	947	100.0	172	4	US-09-245-764-9
4	947	100.0	172	4	US-09-944-277A-13
5	947	100.0	197	2	US-08-756-387B-11
6	947	100.0	197	4	US-09-285-873-11
7	947	100.0	197	4	US-09-944-277A-11
8	947	100.0	232	1	US-07-869-933-13
9	947	100.0	232	2	US-08-756-387B-6
10	947	100.0	232	3	US-09-103-663-13
11	947	100.0	232	4	US-09-285-873-6
12	947	100.0	232	4	US-09-944-277A-6
13	947	100.0	257	1	US-07-869-933-11
14	947	100.0	257	2	US-08-756-387B-2
15	947	100.0	257	3	US-09-103-663-11
16	947	100.0	257	4	US-09-285-873-2
17	947	100.0	257	4	US-08-897-956A-1
18	947	100.0	257	4	US-09-944-277A-2
19	947	100.0	978	4	US-08-897-956A-3
20	941	99.4	197	3	US-08-788-954-2
21	931	98.3	193	5	PCT-US95-08401-1
22	931	98.3	193	5	PCT-US95-08401-1
23	570	60.2	201	3	US-09-015-734-12
24	570	60.2	201	4	US-09-515-311-12
25	570	60.2	236	3	US-09-015-734-7
26	570	60.2	236	4	US-09-515-311-7
27	570	60.2	255	3	US-09-015-734-2

Sequence 2, Appli  
Sequence 14, Appli  
Sequence 31, Appli  
Sequence 4, Appli  
Sequence 28, Appli  
Sequence 24, Appli  
Sequence 20, Appli  
Sequence 9, Appli  
Sequence 9, Appli  
Sequence 10, Appli  
Sequence 13, Appli  
Sequence 13, Appli  
Sequence 12, Appli  
Sequence 12, Appli  
Sequence 12, Appli  
Sequence 7, Appli  
Sequence 7, Appli

28 570 60.2 255 4 US-09-515-311-2  
29 522 55.1 199 3 US-08-833-488B-14  
30 516 54.5 173 3 US-08-833-488B-31  
31 516 54.5 197 3 US-08-833-488B-4  
32 516 54.5 197 3 US-08-833-488B-28  
33 516 54.5 229 3 US-08-833-488B-24  
34 516 54.5 253 3 US-08-833-488B-20  
35 516 54.5 197 3 US-08-833-488B-9  
36 509 53.7 431 4 US-09-592-998C-9  
37 509 53.7 435 4 US-09-592-998C-10  
38 491 51.8 174 2 US-08-768-964-13  
39 491 51.8 174 3 US-09-005-299-13  
40 491 51.8 174 3 US-09-515-431-13  
41 491 51.8 199 2 US-08-768-964-12  
42 491 51.8 199 3 US-09-005-299-12  
43 491 51.8 199 3 US-09-515-431-12  
44 491 51.8 238 2 US-08-768-964-7  
45 491 51.8 238 3 US-09-005-299-7

#### ALIGNMENTS

#### RESULT 1

US-08-756-387B-13  
; Sequence 13, Application US/08756387B  
; Patent No. 5943294  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; APPLICANT: Porter, James P.  
; APPLICANT: Rushlow, Keith E.  
; APPLICANT: Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/756,387B  
; FILING DATE: No. 5945294ember 26, 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 172 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-756-387B-13

Query Match 100.0%; Score 947; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 3e-86;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGEVTLTCGNNFFVSTKXPHNGSLSEETNSSLINIVAKF 60  
Db 1 VPQPKVSLNPPNRIKGEVTLTCGNNFFVSTKXPHNGSLSEETNSSLINIVAKF 60

QY 61 EDSEYKCHQVNESEPVYLFVSDWLLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
 Db 61 EDSEYKCHQVNESEPVYLFVSDWLLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
 QY 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172  
 Db 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

## RESULT 2

US-09-285-873-13  
 ; Sequence 13, Application US/09285873  
 ; Patent No. 6309832  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Frank, Glenn R.  
 ; APPLICANT: Porter, James P.  
 ; APPLICANT: Rushlow, Keith E.  
 ; APPLICANT: Wassom, Donald L.  
 ; TITLE OF INVENTION: Method to Detect Ige  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.  
 ; ADDRESSEE: Heska Corporation  
 ; STREET: 1825 Sharp Point Drive  
 ; CITY: Fort Collins  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80525  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: Wordperfect for Windows, Version 7.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/285,873  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/756,387  
 ; FILING DATE: No. 6309832ember 26, 1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Verser, Carol Talkington  
 ; REGISTRATION NUMBER: 37,459  
 ; REFERENCE/DOCKET NUMBER: DI-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 970/493-7272  
 ; TELEFAX: 970/484-9505  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 172 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-285-873-13

Query Match 100.0%; Score 947; DB 4; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 3e-86;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPQKPKVSLNPPNRIKGENVTLCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60  
 Db 1 VPQKPKVSLNPPNRIKGENVTLCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60  
 QY 61 EDSEYKCHQVNESEPVYLFVSDWLLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
 Db 61 EDSEYKCHQVNESEPVYLFVSDWLLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
 QY 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172  
 Db 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

## RESULT 3

US-09-245-764-9  
 ; Sequence 9, Application US/09245764  
 ; Patent No. 6675105  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hogarth, P. Mark  
 ; APPLICANT: Powell, Maree S.  
 ; APPLICANT: McKenzie, Ian P.C.  
 ; APPLICANT: Maxwell, Kelly P.  
 ; APPLICANT: Garrett, Thomas P.J.  
 ; APPLICANT: Epa, Vidana  
 ; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF PC RECEPTORS  
 ; FILE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: 4102-4  
 ; CURRENT APPLICATION NUMBER: US/09/245,764  
 ; EARLIER APPLICATION NUMBER: 60/099,994  
 ; EARLIER FILING DATE: 1998-09-11  
 ; EARLIER APPLICATION NUMBER: 60/073,972  
 ; EARLIER FILING DATE: 1998-02-06  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 9  
 ; LENGTH: 172  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-245-764-9

Query Match 100.0%; Score 947; DB 4; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 3e-86;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPQKPKVSLNPPNRIKGENVTLCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60  
 Db 1 VPQKPKVSLNPPNRIKGENVTLCNGNNFFVSVSTKWFHNGSLSEETNSSLNIVNAKF 60  
 QY 61 EDSEYKCHQVNESEPVYLFVSDWLLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
 Db 61 EDSEYKCHQVNESEPVYLFVSDWLLLOASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
 QY 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172  
 Db 121 YKDGEALKYWNHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

## RESULT 4

US-09-944-277A-13  
 ; Sequence 13, Application US/09944277A  
 ; Patent No. 6682894  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Frank, Glenn R.  
 ; Porter, James P.  
 ; Rushlow, Keith E.  
 ; Wassom, Donald L.  
 ; TITLE OF INVENTION: Method to Detect Ige  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Carol Talkington Verser, Ph.D.  
 ; ADDRESSEE: Heska Corporation  
 ; STREET: 1825 Sharp Point Drive  
 ; CITY: Fort Collins  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80525  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: Wordperfect for Windows, Version 7.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/944,277A  
 ; FILING DATE: 30-Aug-2001  
 ; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/285,873  
FILING DATE: 1999-03-31  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 197 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-944-277A-13

Query Match 100.0%; Score 947; DB 4; Length 197;  
Best Local Similarity 100.0%; Pred. No. 3.6e-86;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVLTTCGNNFFVSTKWFHNGSLSEETNSSLNIVNAKF 60  
DB 1 VPQPKVSLNPPNRIKGENVLTTCGNNFFVSTKWFHNGSLSEETNSSLNIVNAKF 85  
QY 61 EDSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120  
DB 86 EDSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 145  
QY 121 YKGEALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172  
DB 146 YKGEALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 197

RESULT 6  
US-09-285-873-11  
Sequence 11, Application US/09285873  
Patent No. 6309832  
GENERAL INFORMATION:  
APPLICANT: Frank, Glenn R.  
APPLICANT: Porter, James P.  
APPLICANT: Rushlow, Keith E.  
APPLICANT: Wassom, Donald L.  
TITLE OF INVENTION: Method to Detect Ige  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/285,873  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,387  
FILING DATE: NO. 6309832ember 26, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 197 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-285-873-11

Query Match 100.0%; Score 947; DB 4; Length 197;  
Best Local Similarity 100.0%; Pred. No. 3.6e-86;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/285,873  
FILING DATE: 1999-03-31  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 172 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-944-277A-13

Query Match 100.0%; Score 947; DB 4; Length 172;  
Best Local Similarity 100.0%; Pred. No. 3e-86;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVLTTCGNNFFVSTKWFHNGSLSEETNSSLNIVNAKF 60  
DB 1 VPQPKVSLNPPNRIKGENVLTTCGNNFFVSTKWFHNGSLSEETNSSLNIVNAKF 60  
QY 61 EDSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120  
DB 61 EDSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGWRNDVYKVIY 120  
QY 121 YKGEALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172  
DB 121 YKGEALKYWEHNISITNATVEDSGTYCTGKWQLDYSEPLNITVIKA 172

RESULT 5  
US-08-756-387B-11  
Sequence 11, Application US/08756387B  
Patent No. 5945294  
GENERAL INFORMATION:  
APPLICANT: Frank, Glenn R.  
APPLICANT: Porter, James P.  
APPLICANT: Rushlow, Keith E.  
APPLICANT: Wassom, Donald L.  
TITLE OF INVENTION: Method to Detect Ige  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carol Talkington Verser, Ph.D.  
STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,387B  
FILING DATE: NO. 5945294ember 26, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:

QY 1 VPQKPKVSLNPPNRRIFKGENVTLCNGNRPFEVSTKWFHNGSLSEETNSLSLNIIVNAKF 60  
 Db 26 VPQKPKVSLNPPNRRIFKGENVTLCNGNRPFEVSTKWFHNGSLSEETNSLSLNIIVNAKF 85  
 QY 61 EDGGEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
 Db 86 EDGGEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGRNWDVYKVIY 145  
 QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKQWQDYSEPLNITVIKA 172  
 Db 146 YKDGALKWYENHNISITNATVEDSGTYCTGKQWQDYSEPLNITVIKA 197

## RESULT 7

US-09-944-277A-11  
 ; Sequence 11, Application US/09944277A  
 ; Patent No. 6682894

## GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.  
 Porter, James P.  
 Rushlow, Keith E.  
 Wasson, Donald L.

TITLE OF INVENTION: Method to Detect IGE

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carol Talkington Verser, Ph.D.

STREET: 1825 Sharp Point Drive

CITY: Fort Collins

STATE: Colorado

COUNTRY: USA

ZIP: 80525

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: WordPerfect for Windows, Version 7.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/944,277A

FILING DATE: 30-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/285,873

FILING DATE: 1999-03-31

ATTORNEY/AGENT INFORMATION:

NAME: Verser, Carol Talkington

REGISTRATION NUMBER: 37,459

REFERENCE/DOCKET NUMBER: DI-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 970/493-7272

TELEFAX: 970/484-9505

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 197 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-944-277A-11

Query Match

Best Local Similarity 100.0%; Score 947; DB 4; Length 197;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRRIFKGENVTLCNGNRPFEVSTKWFHNGSLSEETNSLSLNIIVNAKF 60  
 Db 26 VPQKPKVSLNPPNRRIFKGENVTLCNGNRPFEVSTKWFHNGSLSEETNSLSLNIIVNAKF 85

QY 61 EDGGEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

Db 86 EDGGEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGRNWDVYKVIY 145

QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKQWQDYSEPLNITVIKA 172

Db 146 YKDGALKWYENHNISITNATVEDSGTYCTGKQWQDYSEPLNITVIKA 197

Db 146 YKDGALKWYENHNISITNATVEDSGTYCTGKQWQDYSEPLNITVIKA 197

## RESULT 8

US-07-869-933-13

; Sequence 13, Application US/07869933

; Patent No. 5770396

; GENERAL INFORMATION:

APPLICANT: KINET, Jean-Pierre

TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF

THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR

TITLE OF INVENTION: IMMUNOGLOBULIN

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/869,933

FILING DATE: 19920416

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 40399/154 NIHD

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300

TELEFAX: (703)683-4109

TELEX: 899149

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 232 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE:

ORGANISM: homo sapien

STRAIN: FCRI alpha subunit

US-07-869-933-13

Query Match

Best Local Similarity 100.0%; Score 947; DB 1; Length 232;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRRIFKGENVTLCNGNRPFEVSTKWFHNGSLSEETNSLSLNIIVNAKF 60  
 Db 1 VPQKPKVSLNPPNRRIFKGENVTLCNGNRPFEVSTKWFHNGSLSEETNSLSLNIIVNAKF 60

QY 61 EDGGEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

Db 61 EDGGEYKCOHQOVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

QY 121 YKDGALKWYENHNISITNATVEDSGTYCTGKQWQDYSEPLNITVIKA 172

Db 121 YKDGALKWYENHNISITNATVEDSGTYCTGKQWQDYSEPLNITVIKA 172

## RESULT 9

US-08-756-387B-6

; Sequence 6, Application US/08756387B

; Patent No. 5945294

; GENERAL INFORMATION:

APPLICANT: Frank, Glenn R.

APPLICANT: Porter, James P.



```

; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carcl Talkington Verser, Ph.D.
; ADDRESSEE: Heeka Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-756-387B-6

Query Match 100.0%; Score 947; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 4.4e-86;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPWNRIKXGENVLTTCGNFFVSVSTKWFHNGSLSEETNSLINIVNAKF 60
DB 1 VPQKPKVSLNPWNRIKXGENVLTTCGNFFVSVSTKWFHNGSLSEETNSLINIVNAKF 60
QY 61 EDSGYKQCHQOVNESEPVYLEVSDMLLIQSAEVMVGQPLFLCHGWRNWDVYKVYI 120
DB 61 EDSGYKQCHQOVNESEPVYLEVSDMLLIQSAEVMVGQPLFLCHGWRNWDVYKVYI 120
QY 121 YDYGALKYVYENHNISITNATVSDSGTYICTGKWQOLDVSEPLNITVKA 172
DB 121 YDYGALKYVYENHNISITNATVSDSGTYICTGKWQOLDVSEPLNITVKA 172

RESULT 10
US-09-103-663-13
; Sequence 13, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 13
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens

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QY 61 EDGGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
 Db 61 EDGGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120  
 QY 121 YKDGEALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172  
 Db 121 YKDGEALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172

## RESULT 12

US-09-944-277A-6

; Sequence 6, Application US/09944277A

; Patent No. 6682894

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; Porter, James P.

; Rushlow, Keith E.

; Wasson, Donald L.

; TITLE OF INVENTION: Method to Detect Ige

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/944,277A

; FILING DATE: 30-Aug-2001

; CLASSIFICATION: &lt;unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/285,873

; FILING DATE: 1999-03-31

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: DI-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 232 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-944-277A-6

Query Match

Best Local Similarity 100.0%; Score 947; DB 4; Length 232;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTITCGNNFFVSVSTKWFHNGSLSEETNSLNIYNAKF 60

Db 1 VPQPKVSLNPPNRIKGENVTITCGNNFFVSVSTKWFHNGSLSEETNSLNIYNAKF 60

QY 61 EDGGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

Db 61 EDGGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

QY 121 YKDGEALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172

Db 121 YKDGEALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172

## RESULT 13

US-07-869-933-11

; Sequence 11, Application US/07869933

; Patent No. 5770396

; GENERAL INFORMATION:

; APPLICANT: KINET, Jean-Pierre

; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF

; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley &amp; Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/869,933

; FILING DATE: 19920416

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 40399/154 NIHD

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 257 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-869-933-11

Query Match

Best Local Similarity 100.0%; Score 947; DB 1; Length 257;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 26 VPQPKVSLNPPNRIKGENVTITCGNNFFVSVSTKWFHNGSLSEETNSLNIYNAKF 85

QY 61 EDGGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 120

Db 86 EDGGEYKCOHQVNESEPVYLEVFSDDLLOQASAEVVMGQPLFLRCHGRNWDVYKVIY 145

QY 121 YKDGEALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 172

Db 146 YKDGEALKWYENHNISITNATVEDSGTYCTGKWKQLDYSEPLNITVIKA 197

## RESULT 14

US-08-756-387B-2

; Sequence 2, Application US/08756387B

; Patent No. 5945294

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; APPLICANT: Porter, James P.

; APPLICANT: Rushlow, Keith E.

; APPLICANT: Wasson, Donald L.

; TITLE OF INVENTION: Method to Detect Ige

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; ADDRESSEE: Heska Corporation

Db 26 VPQPKVSLNPPWNRIFKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSSLNIVNAKF 85  
Qy 61 EDSGEYKCOHQOVNESEPVYLEVFSDWLLILOASAEVVMGQPLFLRCHGWNRNDVYKVIY 120  
Db 86 EDSGEYKCOHQOVNESEPVYLEVFSDWLLILOASAEVVMGQPLFLRCHGWNRNDVYKVIY 145  
Qy 121 YKDGKALKYWEHNIITNATVEDSGTYCTGKQWOLDYSESEPLNITVIKA 172  
Db 146 YKDGKALKYWEHNIITNATVEDSGTYCTGKQWOLDYSESEPLNITVIKA 197

Search completed: October 6, 2004, 09:04:38  
Job time : 11.2261 secs

STREET: 1825 Sharp Point Drive  
CITY: Fort Collins  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80525  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: WordPerfect for Windows, Version 7.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/756,387B  
FILING DATE: No. 5945294ember 26, 1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Verser, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: DI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 970/493-7272  
TELEFAX: 970/484-9505  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 257 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-756-387B-2

Query Match 100.0%; Score 947; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 5.1e-86;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VPQPKVSLNPPWNRIFKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSSLNIVNAKF 60  
Db 26 VPQPKVSLNPPWNRIFKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSSLNIVNAKF 85  
Qy 61 EDSGEYKCOHQOVNESEPVYLEVFSDWLLILOASAEVVMGQPLFLRCHGWNRNDVYKVIY 120  
Db 86 EDSGEYKCOHQOVNESEPVYLEVFSDWLLILOASAEVVMGQPLFLRCHGWNRNDVYKVIY 145  
Qy 121 YKDGKALKYWEHNIITNATVEDSGTYCTGKQWOLDYSESEPLNITVIKA 172  
Db 146 YKDGKALKYWEHNIITNATVEDSGTYCTGKQWOLDYSESEPLNITVIKA 197

RESULT 15  
US-09-103-663-11  
; Sequence 11, Application US/09103663D  
; Patent No. 6171803  
; GENERAL INFORMATION:  
; APPLICANT: Kinet et al.  
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta  
; TITLE OF INVENTION: subunit of the high affinity receptor for  
; TITLE OF INVENTION: immunoglobulin E.  
; FILE REFERENCE: 50490  
; CURRENT APPLICATION NUMBER: US/09/103,663D  
; CURRENT FILING DATE: 1998-06-23  
; EARLIER APPLICATION NUMBER: 07/869,933  
; EARLIER FILING DATE: 1992-04-16  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-103-663-11

Query Match 100.0%; Score 947; DB 3; Length 257;  
Best Local Similarity 100.0%; Pred. No. 5.1e-86;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 VPQPKVSLNPPWNRIFKGENVTLCNGNNFFEVSTKWFHNGSLSEETNSSLNIVNAKF 60

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:44 ; Search time 52.5221 Seconds  
(without alignments)  
1053.831 Million cell updates/sec

Title: US-10-763-400-13  
Perfect score: 947  
Sequence: 1 VPQKPKVSLNPWNPIFKGE.....GKWLQDYSEPLNITVIKA 172

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*  
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11: /cgn2\_6/prodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/prodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/prodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/prodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/prodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/prodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/prodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/prodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	947	100.0	172	9	US-09-944-277A-13
2	947	100.0	172	9	US-09-245-764-9
3	947	100.0	172	12	US-10-293-992-4
4	947	100.0	172	12	US-10-687-109-9
5	947	100.0	176	10	US-09-809-715-2
6	947	100.0	176	12	US-10-293-992-2
7	947	100.0	197	9	US-09-944-277A-11
8	947	100.0	232	9	US-09-944-277A-6
9	947	100.0	257	9	US-09-944-277A-2
10	947	100.0	257	12	US-10-236-392-28
11	947	100.0	257	14	US-10-384-850-45
12	922	97.4	176	10	US-09-809-715-4
13	714.5	75.4	218	12	US-10-236-392-30
14	570	60.2	201	15	US-10-434-817-12
15	570	60.2	236	15	US-10-434-817-7

16	570	60.2	255	15	US-10-434-817-2
17	376.5	39.8	357	14	US-10-027-736A-9
18	374.5	39.5	336	14	US-10-027-736A-65
19	374.5	39.5	374	12	US-09-836-544-23
20	374.5	39.5	374	14	US-10-027-736A-10
21	371.5	39.2	374	14	US-10-308-279-30
22	371.5	39.2	374	14	US-10-384-850-14
23	369	39.0	404	15	US-10-193-377-7
24	367.5	38.8	399	9	US-09-925-301-1128
25	367.5	38.8	399	14	US-10-106-698-5782
26	366	38.6	254	15	US-10-449-566-117
27	362	38.2	233	15	US-10-193-377-6
28	361	38.1	210	15	US-10-449-566-29
29	361	38.1	254	14	US-10-384-850-44
30	361	38.1	254	14	US-10-027-736A-21
31	361	38.1	254	15	US-10-449-566-116
32	360	38.0	234	14	US-10-027-736A-69
33	360	38.0	254	14	US-10-027-736A-20
34	357	37.7	174	9	US-09-245-764-8
35	357	37.7	174	12	US-10-687-109-8
36	357	37.7	261	9	US-09-245-764-7
37	357	37.7	261	12	US-10-687-109-7
38	353	37.3	298	16	US-10-322-696-93
39	348	36.7	252	14	US-10-027-736A-68
40	348	36.7	294	14	US-10-027-736A-18
41	343	36.2	282	14	US-10-027-736A-66
42	343	36.2	310	14	US-10-027-736A-15
43	339	35.8	281	14	US-10-027-736A-67
44	339	35.8	316	14	US-10-027-736A-17
45	335	35.4	170	9	US-09-245-764-6

## ALIGNMENTS

RESULT 1  
US-09-944-277A-13  
; Sequence 13, Application US/09944/277A  
; Patent No. US2002034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect IGE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; City: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION NUMBER: US/09/944,277A  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 172 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
 US-09-944-277A-13

Query Match 100.0%; Score 947; DB 9; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-78;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPQPKVSLNPPNRIFKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 60  
 DB 1 VPQPKVSLNPPNRIFKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 60  
 QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 DB 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 QY 121 YKDGALKYWNHNISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172  
 DB 121 YKDGALKYWNHNISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172

## RESULT 2

US-09-245-764-9

Sequence 9, Application US/09245764

Patent No. US20020107359A1

GENERAL INFORMATION:

APPLICANT: Hogarth, P. Mark

APPLICANT: Powell, Maree S.

APPLICANT: McKenzie, Ian F.C.

APPLICANT: Maxwell, Kelly F.

APPLICANT: Garrett, Thomas P.J.

APPLICANT: Epa, Vidana

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 4102-4

CURRENT APPLICATION NUMBER: US/09/245,764

CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: 60/099,994

EARLIER FILING DATE: 1998-09-11

EARLIER APPLICATION NUMBER: 60/073,972

EARLIER FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 9

TYPE: PRT

LENGTH: 172

ORGANISM: Homo sapiens

US-09-245-764-9

Query Match 100.0%; Score 947; DB 9; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-78;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPQPKVSLNPPNRIFKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 60  
 DB 1 VPQPKVSLNPPNRIFKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 60  
 QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 DB 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 QY 121 YKDGALKYWNHNISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172  
 DB 121 YKDGALKYWNHNISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172

## RESULT 3

US-10-293-992-4

Sequence 4, Application US/10293992

Publication No. US20040033527A1

GENERAL INFORMATION:

APPLICANT: Jaretzky, Theodore S.

APPLICANT: Garman, Scott Clayton

APPLICANT: Kinet, Jean-Pierre

TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A Fc EPSILON RECEPTOR

TITLE OF INVENTION: CHAIN

FILE REFERENCE: AL-3-CJ-1

CURRENT APPLICATION NUMBER: US/10/293,992

CURRENT FILING DATE: 2002-11-13

PRIOR APPLICATION NUMBER: 09/434,193

PRIOR FILING DATE: 1999-11-04

PRIOR APPLICATION NUMBER: 60/107,219

PRIOR FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patent In version 3.1

SEQ ID NO 4

LENGTH: 172

TYPE: PRT

ORGANISM: Homo sapiens

US-10-293-992-4

Query Match 100.0%; Score 947; DB 12; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-78;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPQPKVSLNPPNRIFKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 60  
 DB 1 VPQPKVSLNPPNRIFKGENVLTTCNGNPFVSVSTKWFHNGSLSEETNSLNIIVNAKF 60  
 QY 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 DB 61 EDGSEYKCOHQOVNESEPVYLEVFSDDLLOASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
 QY 121 YKDGALKYWNHNISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172  
 DB 121 YKDGALKYWNHNISITNATVDSGTYYCTGKWQLDYSEPLNITVIKA 172

## RESULT 4

US-10-687-109-9

Sequence 9, Application US/10687109

Publication No. US20040054480A1

GENERAL INFORMATION:

APPLICANT: Hogarth, P. Mark

APPLICANT: Powell, Maree S.

APPLICANT: McKenzie, Ian F.C.

APPLICANT: Maxwell, Kelly F.

APPLICANT: Garrett, Thomas P.J.

APPLICANT: Epa, Vidana

TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 4102-4

CURRENT APPLICATION NUMBER: US/10/687,109

CURRENT FILING DATE: 2003-10-15

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,764

PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,994

PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,972

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 9

LENGTH: 172

TYPE: PRT

ORGANISM: Homo sapiens

US-10-687-109-9

Query Match 100.0%; Score 947; DB 12; Length 172;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-78;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPWNRIFKGENVTITCNGNNFFVSSSTKWFHNGSLSEETNSSLNINAKF 60  
DB 1 VPQPKVSLNPPWNRIFKGENVTITCNGNNFFVSSSTKWFHNGSLSEETNSSLNINAKF 60  
QY 61 EDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
DB 61 EDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
QY 121 YKDGALKYWTYENHISITNATVEDSGTYTCTGKQWQLDYSEPLNITVIKA 172  
DB 121 YKDGALKYWTYENHISITNATVEDSGTYTCTGKQWQLDYSEPLNITVIKA 172

RESULT 5

US-09-809-715-2  
; Sequence 2, Application US/09809715  
; Publication No. US2003003502A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardtzy, Theodore S.  
; APPLICANT: Garman, Scott Clayton  
; APPLICANT: Wurzburg, Beth A.  
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A FC  
; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A FC REGION OF AN Ige  
; TITLE OF INVENTION: ANTIBODY AND USES THEREOF  
; FILE REFERENCE: AL-8  
; CURRENT APPLICATION NUMBER: US/09/809,715  
; CURRENT FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/189,853  
; PRIOR FILING DATE: 2000-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-715-2

Query Match 100.0%; Score 947; DB 10; Length 176;  
Best Local Similarity 100.0%; Pred. No. 4.3e-78;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VPQPKVSLNPPWNRIFKGENVTITCNGNNFFVSSSTKWFHNGSLSEETNSSLNINAKF 60  
DB 1 VPQPKVSLNPPWNRIFKGENVTITCNGNNFFVSSSTKWFHNGSLSEETNSSLNINAKF 60  
QY 61 EDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
DB 61 EDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
QY 121 YKDGALKYWTYENHISITNATVEDSGTYTCTGKQWQLDYSEPLNITVIKA 172  
DB 121 YKDGALKYWTYENHISITNATVEDSGTYTCTGKQWQLDYSEPLNITVIKA 172

RESULT 6

US-10-293-992-2  
; Sequence 2, Application US/10293992  
; Publication No. US20040033527A1  
; GENERAL INFORMATION:  
; APPLICANT: Jardtzy, Theodore S.  
; APPLICANT: Garman, Scott Clayton  
; APPLICANT: Kinet, Jean-Pierre  
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A FC EPSILON RECEPTOR  
; TITLE OF INVENTION: CHAIN  
; FILE REFERENCE: AL-3-CL-1  
; CURRENT APPLICATION NUMBER: US/10/293,992  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 09/434,193  
; PRIOR FILING DATE: 1999-11-04  
; PRIOR APPLICATION NUMBER: 60/107,219  
; PRIOR FILING DATE: 1998-11-05

; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-992-2

Query Match 100.0%; Score 947; DB 12; Length 176;  
Best Local Similarity 100.0%; Pred. No. 4.3e-78;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VPQPKVSLNPPWNRIFKGENVTITCNGNNFFVSSSTKWFHNGSLSEETNSSLNINAKF 60  
DB 1 VPQPKVSLNPPWNRIFKGENVTITCNGNNFFVSSSTKWFHNGSLSEETNSSLNINAKF 60  
QY 61 EDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
DB 61 EDSGEYKCHQHQVNESEPVYLEVFSDDLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 120  
QY 121 YKDGALKYWTYENHISITNATVEDSGTYTCTGKQWQLDYSEPLNITVIKA 172  
DB 121 YKDGALKYWTYENHISITNATVEDSGTYTCTGKQWQLDYSEPLNITVIKA 172

RESULT 7

US-09-944-277A-11  
; Sequence 11, Application US/09944277A  
; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wasson, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/944,277A  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 197 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-09-944-277A-11

Query Match 100.0%; Score 947; DB 9; Length 197;

Best Local Similarity 100.0%; Pred. No. 4.9e-78;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTLCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60  
Db 26 VPQPKVSLNPPNRIKGENVTLCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 85

QY 61 EDGSEYKCOHQVNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGWRNDVYKVIY 120  
Db 86 EDGSEYKCOHQVNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGWRNDVYKVIY 145

QY 121 YDGEALKWYENHNISITNATVEDSGTYCTGKWQOLDYSEPLNITVIKA 172  
Db 146 YDGEALKWYENHNISITNATVEDSGTYCTGKWQOLDYSEPLNITVIKA 197

RESULT 8  
US-09-944-277A-6  
; Sequence 6, Application US/09944277A  
; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 232 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-944-277A-6

Query Match 100.0%; Score 947; DB 9; Length 232;  
Best Local Similarity 100.0%; Pred. No. 6e-78;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTLCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60  
Db 1 VPQPKVSLNPPNRIKGENVTLCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60

QY 61 EDGSEYKCOHQVNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGWRNDVYKVIY 120

Db 61 EDGSEYKCOHQVNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGWRNDVYKVIY 120

QY 121 YDGEALKWYENHNISITNATVEDSGTYCTGKWQOLDYSEPLNITVIKA 172  
Db 121 YDGEALKWYENHNISITNATVEDSGTYCTGKWQOLDYSEPLNITVIKA 172

RESULT 9  
US-09-944-277A-2  
; Sequence 2, Application US/09944277A  
; Patent No. US20020034771A1  
; GENERAL INFORMATION:  
; APPLICANT: Frank, Glenn R.  
; Porter, James P.  
; Rushlow, Keith E.  
; Wassom, Donald L.  
; TITLE OF INVENTION: Method to Detect Ige  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; FILING DATE: 30-Aug-2001  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/285,873  
; FILING DATE: 1999-03-31  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: DI-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 257 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-944-277A-2

Query Match 100.0%; Score 947; DB 9; Length 257;  
Best Local Similarity 100.0%; Pred. No. 6.8e-78;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQPKVSLNPPNRIKGENVTLCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 60  
Db 26 VPQPKVSLNPPNRIKGENVTLCNGNNFFVSTKWFHNGSLSEETNSLNIVNAKF 85

QY 61 EDGSEYKCOHQVNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGWRNDVYKVIY 120  
Db 86 EDGSEYKCOHQVNESEPVYLEVFSDWLLLOQASAEVVMGQPLFLRCHGWRNDVYKVIY 145

QY 121 YDGEALKWYENHNISITNATVEDSGTYCTGKWQOLDYSEPLNITVIKA 172  
Db 146 YDGEALKWYENHNISITNATVEDSGTYCTGKWQOLDYSEPLNITVIKA 197

RESULT 10  
US-10-236-392-28





```

Best Local Similarity 97.7%; Pred. No. 8.1e-76;
Matches 168; Conservative 0; Mismatches 4; Indels 0; Gaps 0

QY 1 VPQPKVSLNPWNRIKGENVTLTCNGNNFEVSTKWFHNGSLSEETNSSLNIVNAKF 60
Db 1 VPQPKVSLNPWNRIKGENVTLTCNGNNFEVSTKWFHNGSLSEETNSSLNIVNAKF 60

QY 61 EDSGYKCHQCHQVNSEPVIYLFVSDWLLLOASAEVVMGQPLFLRCHGWRNWDYKYVIY 120
Db 61 EDSGYKCHQCHQVNSEPVIYLFVSDWLLLOASAEVVMGQPLFLRCHGWRNWDYKYVIY 120

QY 121 YKDGALKYWNHNHSITNATVEDSGTYCTGKVMQLDYSEPLNITVIKA 172
Db 121 YKDGALKYWNHNHSITNATVEDSGTYCTGKVMQLDYSEPLNITVIKA 172

RESULT 13
US-10-236-392-30
; Sequence 30, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Lakochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Malyankar, Charles E
; APPLICANT: Miller, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:14 : Search time 9.42191 Seconds  
(without alignments)  
1756.007 Million cell updates/sec

Title: US-10-763-400-13  
Perfect score: 947  
Sequence: 1 VPQKPKVSLNPPNRIKGE.....GKVMQDYSEBFLNITVIKA 172

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	947	100.0	257	S00682	IgE Fc receptor al
2	472	49.8	250	A34342	IgE Fc receptor al
3	468	49.4	245	A30154	IgE receptor alpha
4	381	40.2	296	I46021	Fc-gamma receptor
5	371.5	39.2	344	A41357	Fc gamma (1gG) rec
6	371.5	39.2	374	A39878	Fc gamma (1gG) rec
7	371	39.2	280	I55577	Fc gamma (1gG) rec
8	369	39.0	404	A46480	Fc gamma (1gG) rec
9	363.5	38.4	336	I48471	Fc-gamma-1/gamma-2
10	363	38.3	270	A34636	Fc-gamma receptor
11	361	38.1	254	IJ0107	Fc gamma (1gG) rec
12	358	37.8	285	J36903	Fc gamma (1gG) rec
13	357	37.7	233	IJ0284	Fc gamma (1gG) rec
14	354	37.4	283	IJCMSG1	Fc gamma (1gG) rec
15	354	37.4	330	A40071	Fc gamma (1gG) rec
16	354	37.4	330	I49660	Fc-gamma-1/gamma-2
17	353	37.3	267	A35902	Fc gamma (1gG) rec
18	352	37.2	261	I29360	Fc gamma (1gG) rec
19	352	37.2	267	I56110	Fc-gamma RIIB- $\alpha$ p
20	338	35.7	160	I47163	cytolytic trigger
21	338	35.7	267	I27882	Fc gamma receptor
22	335	35.4	323	S06946	Fc gamma (1gG) rec
23	331	35.0	310	IJ0119	Fc gamma (1gG) rec
24	328	34.6	317	IJ0118	Fc gamma (1gG) rec
25	327	34.5	157	I23137	IgE receptor alpha
26	220	23.2	159	I47164	cytolytic trigger
27	161	17.0	1694	S50065	sialoadhesin - mou
28	148	15.6	104	I47165	cytolytic trigger
29	136.5	14.4	458	IWMMSX1	biliary glycoprote

30 136.5 14.4 458 2 JC1509 biliary glycoprote  
31 136.5 14.4 521 2 JC1508 biliary glycoprote  
32 136.5 14.4 521 2 S34338 biliary glycoprote  
33 132 13.9 7962 2 I38346 elastic titin - hu  
34 130 13.7 458 2 S23869 cell-adhesion mole  
35 130 13.7 458 2 S68177 ecto-ATPase protein is  
36 130 13.7 519 2 A44783 non-specific cross-  
37 129.5 13.7 344 2 A27681 neuroglial - fruit  
38 126.5 13.4 1239 1 A32579 vascular cell adhe  
39 125 13.2 538 2 JC2457 immunoglobulin-lik  
40 122 12.9 1327 2 TC9402 protein UNC-89 - C  
41 120 12.7 6642 2 T29757 cell adhesion prot  
42 118 12.5 1033 2 S19247 neural cell adhesi  
43 117 12.4 1197 2 T30581 macrophage colony-  
44 116.5 12.3 978 2 S16385 heparan sulfate pr  
45 116 12.2 3707 2 S18252

ALIGNMENTS

RESULT 1

S00682  
IgE Fc receptor alpha chain precursor - human  
N:Alternate names: Fc-epsilon receptor  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text\_change 23-Jul-1999  
C:Accession: S00682; B30154; S42209  
R:Kochan, J.; Pettine, L.F.; Hakimi, J.; Kishi, K.; Kinet, J.P.  
Nucleic Acids Res. 16, 3584, 1988  
A:Title: Isolation of the gene coding for the alpha subunit of the human high affinity I  
A:Reference number: S00682; MUID:86233953; PMID:2967464  
A:Accession: S00682  
A:Molecule type: mRNA  
A:Residues: 1-257 <KOC>  
A:Cross-references: EMBL:X06948; NID:G31317; PIDN:CAA30025.1; PID:G31318  
R:Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.  
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988  
A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterizat  
A:Reference number: A94191; MUID:88158102; PMID:2964640  
A:Accession: B30154  
A:Molecule type: mRNA  
A:Residues: 1-257 <SHI>  
A:Cross-references: GB:J03605; NID:G187449; PIDN:AAA36204.1; PID:G307164  
R:Yagi, S.; Yanagida, M.; Tanida, I.; Hasegawa, A.; Okumura, K.; Ra, C.  
Eur. J. Biochem. 220, 593-598, 1994  
A:Title: High-level expression of the truncated alpha chain of human high-affinity rece  
nant product.  
A:Reference number: S42209; MUID:94170811; PMID:8125119  
A:Accession: S42209  
A:Molecule type: protein  
A:Residues: 26-197 <YAG>  
A:Experimental source: purified recombinant protein  
C:Genetics:  
A:Gene: GDB:FCER1A  
A:Cross-references: GDB:I19902; OMIM:147140  
A:Map position: Iq23-Iq23  
C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
C:Keywords: immunoglobulin receptor; transmembrane protein  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-257/Product: IgE Fc receptor alpha chain #status predicted <MAT>  
F:44-95/Domain: immunoglobulin homology <IMM1>  
F:125-178/Domain: immunoglobulin homology <IMM2>

Query Match 100.0%; Score 947; DB 2; Length 257;  
Best Local Similarity 100.0%; Pred. No. 7e-70;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPQKPKVSLNPPNRIKGEVTLICGNPNFPEVSTKWFHNGSLSEETNSLNINAKF 60

Db 26 VPQKPKVSLNPPNRIKGEVTLICGNPNFPEVSTKWFHNGSLSEETNSLNINAKF 85

QY 61 EDSGEYKCOHQVNESEPVLEVFSDWLLQLQASAEVMEGQPLFLRCHGRWWDVYKVIY 120

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Db      86 EDGSGYKCHQOVNSESPPVYLFVSDWLLQLQASAEVWVGQPLFLRCHGWRNWDVYKVIY 145
      121 YKDGEALKYWYENHNISITNATVDSGTYCTGKQWQLDYSESEPLNITVIKA 172
      146 YKDGEALKYWYENHNISITNATVDSGTYCTGKQWQLDYSESEPLNITVIKA 197

RESULT 2
A34342
I:Fc receptor alpha chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 23-Jul-1999
C:Accession: A34342; A61238
R:Pa, C.; Jouvin, M.H.E.; Kinet, J.P.
J. Biol. Chem. 264, 15323-15327, 1989
A:Title: Complete structure of the mouse mast cell receptor for IgE (Fc-epsilon-RI) and
A:Reference number: A34342; MUID:89359361; PMID:2527850
A:Accession: A34342
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-250 <RAC>
A:Cross-references: GB:J05018; NID:g193236; PIDN:AAA37600.1; PID:g309224
R:Robertson, M.W.; Mehl, V.S.; Richards, M.L.; Liu, F.T.
Int. Arch. Allergy Appl. Immunol. 96, 289-295, 1991
A:Title: mRNA variants encoding multiple forms of the high-affinity IgE receptor alpha s
A:Reference number: A61238; MUID:92234569; PMID:1839735
A:Accession: A61238
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 125-194 <ROB>
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F:42-94/Domain: immunoglobulin homology <IMM>

Query Match      49.8%; Score 472; DB 2; Length 250;
Best Local Similarity 51.5%; Pred. No. 2.9e-31;
Matches 88; Conservative 35; Mismatches 46; Indels 2; Gaps 2;

QY      3 QKPXVSLNPPWNRIFKGENVTLCNGNFFEV-SSTKWFHNGSLSEETNSLINVAKPE 61
      26 EKSVTLDPPIRIFTEGKVTLSYGNHLOQMSITKWIHNGTVSEVNSHLVIVSATVQ 85
QY      62 DSGYKCHQOVNSESPPVYLFVSDWLLQLQASAEVWVGQPLFLRCHGWRNWDVYKVIY 121
      86 DSGYKICQKQGLFKSPVYLVNTQDMLLQTSADMLVHGSFDIRCHGWKWNVRKVIY 145
QY      122 KDGEALKYWYENHNISITNATVDSGTYCTGKQWQLDYSESEPLNITVIKA 172
      146 RNDHAFNYSYES-PVSIREATLNDSGTYHCKGYLRQVEYSDKFRIVAVKA 195

RESULT 3
A30154
I:Fc receptor alpha chain precursor - rat
N:Alternate names: Fc-epsilon-R alpha chain precursor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jan-2000
C:Accession: C31327; A31327; A30154; A27116; I55304
R:Liu, F.T.; Albrandt, K.; Robertson, M.W.
Proc. Natl. Acad. Sci. U.S.A. 85, 5639-5643, 1988
A:Title: cDNA heterogeneity suggests structural variants related to the high-affinity Ig
A:Reference number: A94203; MUID:88289772; PMID:2969594
A:Accession: C31327
A:Molecule type: mRNA
A:Residues: 1-245 <LIU>
A:Cross-references: GB:M21622; GB:J03811
A:Experimental source: basophilic leukemia cell line, clone R3-4
A:Accession: A31327
A:Molecule type: mRNA
A:Residues: 21-245 <LI3>
A:Cross-references: GB:M21622; NID:g204109; PIDN:AAA41146.1; PID:g204110; GB:J03811
A:Experimental source: basophilic leukemia cell line

```

```

R;Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
A:Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterizati
A:Reference number: A94191; MUID:88158102; PMID:2964640
A:Accession: A30154
A:Molecule type: mRNA
A:Residues: 1-245 <SHI>
A:Cross-references: GB:J03606; NID:g205331; PIDN:AAA41582.1; PID:g205332
R;Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.
Biochemistry 26, 4605-4610, 1987
A:Title: A cDNA presumptively coding for the alpha subunit of the receptor with high affi
A:Reference number: A27116; MUID:88024987; PMID:2959318
A:Accession: A27116
A:Molecule type: mRNA
A:Residues: 1-G', 3-236, N', 238-244, 'RLKPNS' <KIN>
R;Tepler, I.; Shimizu, A.; Leder, P.
J. Biol. Chem. 264, 5912-5915, 1989
A:Title: The gene for the rat mast cell high affinity IgE receptor alpha chain. Structur
A:Reference number: I55304; MUID:89174653; PMID:2522441
A:Accession: I55304
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RES>
A:Cross-references: GB:M25334; NID:g341335; PIDN:AAA74562.1; PID:g556391
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-245/Product: IgE receptor alpha chain #status predicted <MAT>
F:42-93/Domain: immunoglobulin homology <IMM>

Query Match      49.4%; Score 468; DB 2; Length 245;
Best Local Similarity 50.9%; Pred. No. 6e-31;
Matches 86; Conservative 33; Mismatches 50; Indels 0; Gaps 0;

QY      3 QKPXVSLNPPWNRIFKGENVTLCNGNFFEVSTKWFHNGSLSEETNSLINVAKPED 62
      26 QKSVVSLDPPPIRITLTDGKVTLCNGNNSQMSQNTKWIHNDISNKKSHWVIVSATIQD 85
QY      63 SGEYKCHQOVNSESPPVYLFVSDWLLQLQASAEVWVGQPLFLRCHGWRNWDVYKVIY 122
      86 SGKYICQKQGYKSPVYLVNWQEWLLOSSADVLDNGSFDIRCSWKKWKHKVIY 145
QY      123 DGEALKYWYENHNISITNATVDSGTYCTGKQWQLDYSESEPLNITVIK 171
      146 DDIAPKYSYDSNNISIRKATFNDSGTYHCTGYLNKVECKSDKFSIAVVK 194

RESULT 4
I46021
Fc-gamma receptor II - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 23-Jul-1999
C:Accession: I46021; S40204
R;Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.
Immunogenetics 39, 423-427, 1994
A:Title: Cattle Fc gamma RI: molecular cloning and ligand specificity.
A:Reference number: I46021; MUID:94245284; PMID:8188320
A:Accession: I46021
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-296 <ZHA>
A:Cross-references: EMBL:X75671; NID:g437978; PIDN:CAA53367.1; PID:g437979
C:Superfamily: Fc gamma receptor III; immunoglobulin homology
C:Keywords: immunoglobulin receptor

Query Match      40.2%; Score 381; DB 2; Length 296;
Best Local Similarity 41.2%; Pred. No. 8.8e-24;
Matches 70; Conservative 33; Mismatches 65; Indels 2; Gaps 1;

QY      2 PQPKK--VSLNPPWNRIFKGENVTLCNGNFFEVSTKWFHNGSLSEETNSLINVAK 59
      44 PDLKAVVTQPAWVNLVREDVLTLCQGTSGAGNLTTFHNGSIHTQKQPSYFRAG 103

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A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-280 <RES>  
 A:Cross-references: GB:L03419; NID:g182460; PIDN:AAA35825.1; PID:g292023  
 A>Note: splice form B1  
 A:Accession: I70303  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-10,103-153 'A',155-280 <RE2>  
 A:Cross-references: GB:L03420; NID:g182461; PIDN:AAA35826.1; PID:g292024  
 A:Experimental source: mononuclear cells  
 A>Note: splice form B2  
 A:Comment: This receptor does not bind monomeric IgG with high affinity.  
 C:Genetics:  
 A:Gene: GDB:FCGR1B; CD64  
 A:Cross-references: GDB:135923; OMIM:601502  
 A:Map position: lp12-lp12  
 C:Superfamily: Fc gamma receptor I; immunoglobulin homology  
 C:Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane P  
 F:117-170/Domain: immunoglobulin homology <IMM>

Query Match 39.2%; Score 371; DB 2; Length 280;  
 Best Local Similarity 43.3%; Pred. No. 5.4e-23; Indels 0; Gaps 0;  
 Matches 65; Conservative 32; Mismatches 53;

QY 4 KPVSLNPPWNRIPKGENVTITCNNGNFFVSSSTKWFHNGSLSEETNSLNINAKPEDS 63  
 DB 21 KAVITLQPPWVSFQETVTILHCEVLHPGSSSTQWFNGTATQTSTPSYRITSASVND 80  
 QY 64 GEYKCOHQVNESEPVYLEVFSQAEVVMGQPLFLRCHGRWMDVYKVIYKD 123  
 DB 81 GEYKQRLGSRSDPIQELHGRWLLQVSSRFMEGEPLALRCHAWKOLVNVLYRN 140  
 QY 124 GEALKYWEHNHISITNATVEDSGTYCTG 153  
 DB 141 GKAFKFFHNSNLITKLNISHNGTYHCSG 170

RESULT 8  
 A46480  
 Fc gamma (IgG) receptor high affinity - mouse  
 A:Alternative names: high affinity IgG receptor  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: A46480; A43511  
 R:Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.  
 J. Immunol. 148, 1570-1575, 1992  
 A:Title: Structure and mapping of the gene encoding mouse  
 A:Reference number: A46480; MUID:92166399; PMID:1531670  
 A:Accession: A46480  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-404 <OSM>  
 A>Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85212, NC  
 R:Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.  
 J. Immunol. 144, 371-378, 1990  
 A:Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG  
 A:Reference number: A43511; MUID:90111035; PMID:2136886  
 A:Accession: A43511  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-404 <SEA>  
 A:Cross-references: GB:M31314; NID:g200752; PIDN:AAA40056.1; PID:g200753  
 C:Superfamily: Fc gamma receptor I; immunoglobulin homology  
 C:Keywords: immunoglobulin receptor; transmembrane protein  
 F:127-179/Domain: immunoglobulin homology <IMM>

Query Match 39.0%; Score 369; DB 2; Length 404;  
 Best Local Similarity 43.4%; Pred. No. 1.2e-22;  
 Matches 72; Conservative 35; Mismatches 57; Indels 2; Gaps 2;

QY 4 KPVSLNPPWNRIPKGENVTITCNNGNFFVSSSTKWFHNGSLSEETNSLNINAKPEDS 63  
 DB 21 KAVITLQPPWVSFQETVTILHCEVLHPGSSSTQWFNGTATQTSTPSYRITSASVND 80  
 QY 64 GEYKCOHQVNESEPVYLEVFSQAEVVMGQPLFLRCHGRWMDVYKVIYKD 123  
 DB 81 GEYKQRLGSRSDPIQELHGRWLLQVSSRFMEGEPLALRCHAWKOLVNVLYRN 140  
 QY 124 GEALKYWEHNHISITNATVEDSGTYCTG 153  
 DB 141 GKAFKFFHNSNLITKLNISHNGTYHCSG 170

Db 31 KAVITLQPPWVSIFOKENVTLNCEGPHLPDGSSTQWFNGTAVQISTPSYSIPASFDQS 90  
 QY 64 GEYKCOHQVNESEPVYLEVFSQAEVVMGQPLFLRCHGRWMDVYKVIYKD 123  
 Db 91 GEYRCQIGSSVSPDPVQLQIHNDWLLQASREVLTGEPEPLALRCHGWKNKLVNVVYFVRN 150  
 QY 124 GEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITV 169  
 Db 151 GKSQFQ-SSDSEVALKTNLSHSGIYHCSG-TGRHRYTSAGVSITV 194

RESULT 9  
 A49471  
 Fc gamma (IgG) receptor high affinity - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jan-2000  
 C:Accession: I48471  
 R:Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Caff  
 A:Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig  
 A:Reference number: I48471; MUID:93242399; PMID:8480181  
 A:Accession: I48471  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-336 <RES>  
 A:Cross-references: EMBL:X70980; NID:g311748; PIDN:CAA50311.1; PID:g311749  
 C:Superfamily: Fc gamma receptor I; immunoglobulin homology  
 C:Keywords: immunoglobulin receptor  
 F:128-180/Domain: immunoglobulin homology <IMM>

Query Match 38.4%; Score 363.5; DB 2; Length 336;  
 Best Local Similarity 44.3%; Pred. No. 2.7e-22;  
 Matches 74; Conservative 33; Mismatches 57; Indels 3; Gaps 3;

QY 4 KPVSLNPPWNRIPKGENVTITCNNGNFFVSSSTKWFHNGSLSEETNSLNINAKPEDS 63  
 Db 31 KAVITLQPPWVSIFOKENVTLNCEGPHLPDGSSTQWFNGTAVQISTPSYSIPASFDQS 90  
 QY 64 GEYKCOHQVNESEPVYLEVFSQAEVVMGQPLFLRCHGRWMDVYKVIYKD 122  
 Db 91 GEYRCQIGSSVSPDPVQLQIHNDWLLQASREVLTGEPEPLALRCHGWKNKLVNVVYFVR 150  
 QY 123 DEALKYWEHNHISITNATVEDSGTYCTGKQWQLDYSEPLNITV 169  
 Db 151 NGSFPR-SGSKIALKTNLSHSGIYHCSG-MGRHRYTSAGVSITV 195

RESULT 10  
 A34636  
 Fc-gamma receptor II precursor - guinea pig  
 C:Species: Cavia porcellus (guinea pig)  
 C:Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 16-Jul-1999  
 C:Accession: A34636  
 R:Tominaga, M.; Sakata, A.; Ohmura, T.; Yamashita, T.; Koyama, J.; Onoue, K.  
 Biochem. Biophys. Res. Commun. 168, 683-689, 1990  
 A:Title: The structure and expression of the guinea pig Fc receptor for IgG1 and IgG2 (F  
 A:Reference number: A34636; MUID:90241239; PMID:1692213  
 A:Accession: A34636  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-270 <TOM>  
 A:Cross-references: GB:M35272  
 C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
 C:Keywords: immunoglobulin receptor  
 F:37-88/Domain: immunoglobulin homology <IMM>

Query Match 38.3%; Score 363; DB 2; Length 270;  
 Best Local Similarity 43.5%; Pred. No. 2.3e-22;  
 Matches 73; Conservative 21; Mismatches 74; Indels 0; Gaps 0;

QY 2 POKPVSLNPPWNRIPKGENVTITCNNGNFFVSSSTKWFHNGSLSEETNSLNINAKFE 61  
 Db 20 PPKAVVLEPPWQVLRGDRVTLTCEGAPSGFNHSTQWLNHGRLLIPTQVLPFSYRFTAKGN 79



QY 62 DSGEYKCOHQVNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIYY 121  
Db 80 DSGEYRCQAGTSLSDPVELDVISDWLVLTQSLIFQEGDVLVLRCHSWNNWFLAKVTFY 139  
QY 122 KGGEALKYENHNISITNATVEDSGTYCTGKWQWLDYESEPLNITV 169  
Db 140 HNGVAKYFISKNFSPONASHSGAYNCTGLIGRTSHTSPVITV 187  
RESULT 11  
JL0107  
Fc gamma (IgG) receptor III-A precursor (natural killer cell) [validated] - human  
N;Alternate names: CD16 antigen; low affinity IgG Fc receptor type III-2 precursor; surf  
C;Species: Homo sapiens (man)  
C;Date: 07-Sep-1990 #sequence revision 02-Aug-1996 #text\_change 08-Dec-2000  
C;Accession: J0107; A50383; A32933; I37627  
R;Avatch, J.V.; Perussia, B.  
J. Exp. Med. 170, 481-497, 1989  
A;Title: Alternative membrane forms of Fc gamma RIIII(CD16) on human natural killer cells  
A;Reference number: JL0107; MUID:89328325; PMID:2526846  
A;Accession: JL0107  
A;Molecule type: mRNA  
A;Residues: 1-254 <RAV>  
A;Cross-references: GB:X52645; GB:M31937; NID:G31323; PIDN:CAA36870.1; PID:G31324  
A;Note: the sequence of the receptor from human polymorphonuclear granulocytes, reported  
21 residues  
R;Trounstine, M.L.; Peltz, G.A.; Yssel, H.; Huizinga, T.W.J.; von dem Borne, A.E.G.K.; S  
Int. Immunol. 2, 303-310, 1990  
A;Title: Reactivity of cloned, expressed human Fc gammaRIII isoforms with monoclonal anti  
A;Reference number: A60383; MUID:91120527; PMID:1703781  
A;Accession: A60383  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-254 <TRO>  
R;Scallion, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C  
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989  
A;Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phosph  
A;Reference number: A32933; MUID:89236947; PMID:2525780  
A;Accession: A32933  
A;Molecule type: mRNA  
A;Residues: 31-254 <SCA>  
A;Cross-references: GB:M24853; NID:G184849; PIDN:AAA53506.1; PID:G386806  
R;Gessner, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E.  
J. Biol. Chem. 270, 1350-1361, 1995  
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole  
A;Reference number: A55439; MUID:95138131; PMID:7836402  
A;Accession: I37627  
A;Molecule type: DNA  
A;Residues: 1-39 <RES>  
A;Cross-references: EMBL:Z46222; NID:9559445; PIDN:CAA86295.1; PID:G1478198  
A;Note: translation has been corrected relative to PID:G871305  
C;Comment: This low affinity IgG Fc receptor of natural killer cells, which is the produ  
e nearly identical, yet this receptor lacks a glycosylphosphatidylinositol anchor and in  
C;Genetics:  
A;Gene: GDB:FCGR3A; FCGR3  
A;Cross-references: GDB:I19904; OMIM:146740  
A;Map position: 1q23-1q23  
A;Introns: 14/1; 21/1  
A;Note: the list of introns is incomplete  
C;Superfamily: Fc gamma receptor III; immunoglobulin homology  
C;Keywords: glycoprotein; receptor; transmembrane protein  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-254/Product: Fc gamma (IgG) receptor III-A #status experimental <MAT>  
F;18-208/Domain: extracellular #status predicted <EXT>  
F;40-91/Domain: immunoglobulin homology <IMM>  
F;11-174/Domain: immunoglobulin homology <IMM2>  
F;209-229/Domain: transmembrane #status predicted <TRZ>  
F;230-254/Domain: intracellular #status predicted <CYT>  
F;56,63,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.1%; Score 361; DB 1; Length 254;  
Best Local Similarity 44.0%; Pred. NO. 3.1e-22;

Matches 73; Conservative 26; Mismatches 67; Indels 0; Gaps 0;  
QY 4 KPKVSLNPPNRRFKGENVTITCNGNNFFVSVSTKTFHNGSLSEETNSLINIVAKPEDS 63  
Db 25 KAVVLEPQYRYLEKDSVTLKCGAYSPEDNSTQMFHNSLSSQASSYFIDAATVDDS 84  
QY 64 GEYKCOHQVNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIYYKD 123  
Db 85 GEYRCQINLSTLSDPVQLEVHIGWLLQLQAPRWVKEEDPHLRCHSWKNTALHKVTLQ 144  
QY 124 GEALKYENHNISITNATVEDSGTYCTGKWQWLDYESEPLNITV 169  
Db 145 KGGRKYFHNSDFYIPKATLKDGSYFCRGLFGSKNVSSETVAITI 190

## RESULT 12

S36903

Fc gamma (IgG) receptor type 2 precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Jan-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C;Accession: S36903

R;Boeck, P.; Pecht, I.

FEBS Lett. 331, 86-90, 1993

A;Title: Cloning and sequence of the cDNA coding for rat type II Fc-gamma receptor of ma

A;Reference number: S36903; MUID:94009652; PMID:8405417

A;Accession: S36903

A;Molecule type: mRNA

A;Residues: 1-285 &lt;BOC&gt;

A;Cross-references: EMBL:X73371; NID:G37576; PIDN:CAA51788.1; PID:G37577

C;Superfamily: Fc gamma receptor III; immunoglobulin homology

C;Keywords: immunoglobulin receptor

F;52-103/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 37.8%; Score 358; DB 2; Length 285;

Best Local Similarity 40.4%; Pred. NO. 6.3e-22;

Matches 67; Conservative 33; Mismatches 66; Indels 0; Gaps 0;

QY 4 KPKVSLNPPNRRFKGENVTITCNGNNFFVSVSTKTFHNGSLSEETNSLINIVAKPEDS 63

Db 37 KAVVLEPQYRYLEKDSVTLKCGAYSPEDNSTQMFHNSLSSQASSYFIDAATVDDS 96

QY 64 GEYKCOHQVNESEPVYLEVFSWLLQLQASAEVVMGQPLFLRCHGWRNWDVYKVIYYKD 123

Db 97 GEYRCRMSETGISEPHLGVISDWLLQTSQIVVEGETITLRCCHSWKNTALHKVTLQ 156

QY 124 GEALKYENHNISITNATVEDSGTYCTGKWQWLDYESEPLNITV 169

Db 157 GKPVRVYHQSSNFSIPKANHSNGNYCKAYLGRTHMVSKEPTITV 202

## RESULT 13

JU0284

Fc gamma (IgG) receptor III-B precursor (neutrophil) - human

N;Alternate names: FcR III; IgG Fc receptor precursor, type III-1 (polymorphonuclear gra

C;Species: Homo sapiens (man)

C;Date: 07-Sep-1990 #sequence\_revision 02-Aug-1996 #text\_change 28-Jan-2000

C;Accession: JU0284; S00758; I37628; B32933; A31460

R;Avatch, J.V.; Perussia, B.

J. Exp. Med. 170, 481-497, 1989

A;Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells

A;Reference number: JL0107; MUID:89328325; PMID:2526846

A;Accession: JU0284

A;Molecule type: mRNA

A;Residues: 1-201, 204-233 &lt;RAV&gt;

A;Cross-references: GB:J04162

A;Note: the sequence of the receptor from human NK cells, reported in the same paper, d

rboxyl end

R;Simmons, D.; Seed, B.

Nature 333, 568-570, 1988

A;Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane

A;Reference number: S00758; MUID:89232937; PMID:2967436

A;Accession: S00758

A;Molecule type: mRNA

A:Residues: 1-233 <SIM>  
A:Cross-references: EMBL:X07934; NID:G29744; PIDN:CAA30758.1; PID:G29745  
R:Gessner, J.E.; Grussemeyer, T.; Kolanus, W.; Schmidt, R.E.  
J. Biol. Chem. 270, 1350-1361, 1995  
A:Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole  
A:Reference number: A55439; MUID:95138131; PMID:7836402  
A:Accession: I37628  
A:Molecule type: DNA  
A:Residues: 1-72 <RES>  
A:Cross-references: EMBL:Z46223; NID:G559446; PIDN:CAA86296.1; PID:9871306  
R:Scallan, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989  
A:Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phos  
A:Reference number: A32933; MUID:89296947; PMID:2525780  
A:Accession: B32933  
A:Molecule type: mRNA  
A:Residues: 1-121, 'E', 123-150, 'S', 152-233 <SCA>  
A:Cross-references: GB:M24854; NID:G184851; PIDN:AA53507.1; PID:G306930  
R:Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W.  
Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989  
A:Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal  
A:Reference number: A31460; MUID:89128838; PMID:2521732  
A:Accession: A31460  
A:Molecule type: mRNA  
A:Residues: 37-64, 'N', 66-81, 'D', 83-105, 'V', 107-233 <PEL>  
A:Cross-references: GB:J04162; NID:G183036; PIDN:AA35881.1; PID:G183037  
C:Comment: This low affinity IGG Fc receptor of neutrophils, which is the product of the  
I, yet this receptor lacks 21 residues at the carboxyl end because of an early stop cod  
C:Genetics:  
A:Gene: GDB:FCGR3B; FCGR3  
A:Cross-references: GDB:128176; OMIM:146740  
A:Map position: 1q23-1q23  
A:Introns: 14/1; 21/1  
A:Note: the list of introns is incomplete  
C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-203/Product: Fc gamma (IgG) receptor III-B #status predicted <MAT>  
F:40-91/Domain: immunoglobulin homology <IMM1>  
F:111-174/Domain: immunoglobulin homology <IMM2>  
F:563,82,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match 37.7%; Score 357; DB 1; Length 233;  
Best Local Similarity 44.0%; Pred. No. 6e-22;  
Matches 73; Conservative 25; Mismatches 68; Indels 0; Gaps 0;  
QY 4 KPKVSLNPPNRIKGENVTITCNNGNFFVSSSTKWFHNGSLSEETNSSLINIVNAKPEDS 63  
DB 25 KAVVLEFPQVSVLEKDSVTLKCGAYSPEDNSTOWPHNESLSSQASSYFIDAATVND 84  
QY 64 GEYKCOHQVNEBPVYLFVSDWLLLOQAEVVMGQPLFLRCHGRWMDVYKVIYKD 123  
DB 85 GEYFCQNLSTLSDPQVLEHIGWLLLOQAPRWVFKEDPDLRCHGRWMDVYKVIYQN 144  
QY 124 GEALKYWEHNHISITNATVEDSGTYCTGKVMQDYSEPLNITV 169  
DB 145 GKDRKYFHNSDFHPRATLKGSGSYFCRGLVGSKNVSETNITI 190

RESULT 14  
FCMSG1  
Fc gamma (IgG) receptor II (low affinity) beta (splice form 2) precursor - mouse  
N:Alternate names: macrophage-lymphocyte IgG1/IgG2b Fc receptor  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1989 #sequence revision 16-Aug-1996 #text change 10-Sep-1999  
A:Accession: B40071; S29362; A93384; A94125; A25741; A25501  
R:Hogarth, P.M.; Witort, E.; Hulett, M.D.; Bonnerot, C.; Even, J.; Fridman, W.H.; McKenz  
J. Immunol. 146, 369-376, 1991  
A:Title: Structure of the mouse beta2fcgamma receptor II gene.  
A:Reference number: A40071; MUID:91079576; PMID:1824594  
A:Accession: B40071  
A>Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-283 <HOG>  
R:Ravech, J.V.; Luster, A.D.; Weinshank, R.; Kochan, J.; Pavlovic, A.; Portnoy, D.A.; H  
Science 234, 718-725, 1986  
A:Title: Structural heterogeneity and functional domains of murine immunoglobulin G Fc r  
A:Reference number: S29360; MUID:87042761; PMID:2946078  
A:Accession: S29362  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-283 <RAV>  
A:Cross-references: EMBL:W14216; NID:G193258; PIDN:AAA37609.1; PID:G309231  
R:Lewis, V.A.; Koch, T.; Plutner, H.; Wellman, I.  
Nature 324, 372-375, 1986  
A:Title: A complementary DNA clone for a macrophage-lymphocyte Fc receptor.  
A:Reference number: A93384; MUID:87065089; PMID:3024012  
A:Accession: A93384  
A:Molecule type: mRNA  
A:Residues: 17-283 <LEW>  
R:Hibbs, M.L.; Walker, I.D.; Kirszbaum, L.; Pietersz, G.A.; Deacon, N.J.; Chambers, G.W.  
Proc. Natl. Acad. Sci. U.S.A. 83, 6980-6984, 1986  
A:Title: The murine Fc receptor for immunoglobulin: purification, partial amino acid seq  
A:Reference number: A94125; MUID:86313694; PMID:2944118  
A:Accession: A94125  
A:Molecule type: mRNA  
A:Residues: 17-45; 255-277 <HIB>  
A:Note: parts of this sequence, including the amino end of the mature protein, were dete  
C:Genetics:  
A:Map position: 1  
C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; immunoglobulin receptor; tr  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:30-283/Product: Fc gamma receptor II beta, form 2 #status predicted <MAT>  
F:50-101/Domain: immunoglobulin homology <IMM1>  
F:131-184/Domain: immunoglobulin homology <IMM2>  
F:209-236/Domain: transmembrane #status predicted <TM>  
F:237-283/Domain: intracellular #status predicted <INT>  
F:57-99,138-182/Disulfide bonds: #status predicted  
F:65,92,166,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.4%; Score 354; DB 1; Length 283;  
Best Local Similarity 41.9%; Pred. No. 1.3e-21;  
Matches 70; Conservative 32; Mismatches 63; Indels 2; Gaps 2;  
QY 4 KPKVSLNPPNRIKGENVTITCNNGNFFVSSSTKWFHNGSLSEETNSSLINIVNAKPE 62  
DB 35 KAVVLEFPQVSVLEKDSVTLKCGAYSPEDNSTOWPHNESLSSQASSYFIDAATVND 93  
QY 63 SGEYKCOHQVNEBPVYLFVSDWLLLOQAEVVMGQPLFLRCHGRWMDVYKVIYK 122  
DB 94 SGEYFCQMEQFLSDPVDLGVISDWLLLOQAPRWVFKEDPDLRCHGRWMDVYKVIYK 153  
QY 123 DEALKYWEHNHISITNATVEDSGTYCTGKVMQDYSEPLNITV 169  
DB 154 NEKSVRYHHYGSNFSIPKANHSKSHSGDYCKGSLGRTLLHQSKPVTITV 200

RESULT 15  
A40071  
Fc gamma (IgG) receptor II (low affinity) beta (splice form 1) precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Mar-1992 #sequence revision 06-Mar-1992 #text change 23-Jul-1999  
A:Accession: A40071; A60761; S29361  
R:Hogarth, P.M.; Witort, E.; Hulett, M.D.; Bonnerot, C.; Even, J.; Fridman, W.H.; McKenz  
J. Immunol. 146, 369-376, 1991  
A:Title: Structure of the mouse beta2fcgamma receptor II gene.  
A:Reference number: A40071; MUID:91079576; PMID:1824594  
A:Accession: A40071  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-330 <HOG>  
A:Cross-references: GB:M63284; NID:G192161; PIDN:AAA37289.1; PID:G192163  
R:Lah, M.; Quelch, K.; Deacon, N.J.; McKenzie, I.F.C.; Hogarth, P.M.  
Immunogenetics 31, 202-206, 1990

A>Title: Identification of the mouse beta 2-microglobulin polymorphism by direct sequencing  
A:Reference number: A60761; MUID:90202030; PMID:2138587  
A:Accession: A60761  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-144, 'P', 146-189, 'Q', 191-298, 'P', 300-330 cLAH>  
A:Cross-references: GB:IM3131; MID:G1932260; PIDN:AAA37610.1; PID:G397155  
R:Ravetch, J.V.; Luster, A.D.; Weinshank, R.; Kochan, J.; Pavlovic, A.; Portnoy, D.A.; H  
Science 234, 718-725, 1986  
A>Title: Structural heterogeneity and functional domains of murine immunoglobulin G Fc  
A:Reference number: S29360; MUID:87042761; PMID:2946078  
A:Accession: S29361  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-269, 'L', 271, 'A', 'C', 276, 'R', 279-330 <RAV>  
A:Cross-references: EMBL:M16367; NID:G193256; PIDN:AAA37608.1; PID:G309230  
C:Superfamily: Fc gamma receptor III; immunoglobulin homology  
C:Keywords: immunoglobulin receptor  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:50-101/Domain: immunoglobulin homology <IMM1>  
F:131-184/Domain: immunoglobulin homology <IMM2>

Query Match 37.4%; Score 354; DB 2; Length 330;  
Best Local Similarity 41.9%; Pred. No. 1.6e-21;  
Matches 70; Conservative 32; Mismatches 63; Indels 2; Gaps 2;

QY 4 KPKVSLNPWNRIKGEKNTVLICNGNFFEVSTKWFHNG-SLSBETNSSLNIVAKPED 62  
Db 35 KAVVLEPPMIQVLKEDTTLTCGTHNPGNSITQWFHNGSIRSOVQASYTF-KATVND 93  
QY 63 SGYKQCHQWNESEFPVILEFSDMLLQASAEVNVNMGOPFLIRCHGMWNWDVYKVIYK 122  
Db 94 SGYRQMEGTRLSDFVDLCVLSDDLQLLTQPOLVFLFEGETITLRCHEWKNLLNRISSPH 153  
QY 123 DGEALXYWENHNISITNATVEDSGYTYCTGKVKWQLDYESEPLNITV 169  
Db 154 NEKSVRYHYHNSNFSIPKANHSHGDIYKGSIGLRTLHQS KPVITV 200

Search completed: October 6, 2004, 09:23:44  
Job time : 10.4219 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:39 ; Search time 5.81352 Seconds  
(without alignments)  
1540.558 Million cell updates/sec

Title: US-10-763-400-13

Perfect score: 947  
Sequence: 1 VFQKPKVSLNPPNRFKGE.....GKWLQDYSEPLNITVKA 172

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	947	100.0	257	1 FCEA_HUMAN	P12319 homo sapien
2	472	49.8	250	1 FCEA_MOUSE	P20489 mus musculus
3	468	49.4	245	1 FCE1_RAT	P12371 rattus norv
4	381	40.2	296	1 FCG2_BOVIN	Q28110 bos taurus
5	374.5	39.5	374	1 FCG1_HUMAN	P12314 homo sapien
6	369	39.0	404	1 FCG1_MOUSE	P26151 mus musculus
7	365	38.5	250	1 FCG3_BOVIN	P79107 bos taurus
8	363	38.3	341	1 FCG2_CAVPO	Q60513 cavia porce
9	361	38.1	254	1 FCG3_HUMAN	P08637 homo sapien
10	360	38.0	257	1 FCG3_PIG	Q28942 sus scrofa
11	358	37.8	285	1 FCG2_RAT	Q63203 rattus norv
12	357	37.7	233	1 FCG3_HUMAN	O75015 homo sapien
13	354	37.4	330	1 FCG2_MOUSE	P08101 mus musculus
14	353	37.3	267	1 FCG3_RAT	P27645 rattus norv
15	352	37.2	261	1 FCG3_MOUSE	P08508 mus musculus
16	339	35.8	316	1 FCGA_PANTR	Q8SPV8 pan troglod
17	335	35.4	310	1 FCG3_HUMAN	P31994 homo sapien
18	335	35.4	323	1 FCGC_HUMAN	P31995 homo sapien
19	328	34.6	317	1 FCGA_HUMAN	P12318 homo sapien
20	327	34.5	157	1 FCE2_RAT	P12840 rattus norv
21	166.5	17.6	1709	1 SN_HUMAN	Q9B222 homo sapien
22	161	17.0	1694	1 SN_MOUSE	Q62230 mus musculus
23	152	16.1	422	1 K3L1_RAT	P83555 rattus norv
24	144	15.2	432	1 K3L1_MOUSE	P83555 mus musculus
25	136.5	14.4	521	1 CFEAL_MOUSE	P31809 mus musculus
26	133.5	14.1	837	1 NCM2_MOUSE	Q35136 mus musculus
27	130	13.7	519	1 ECTO_RAT	P16573 rattus norv
28	128.5	13.6	344	1 CBAE_HUMAN	P40199 homo sapien
29	126.5	13.4	1302	1 NFG_DROME	P20241 drosophila
30	120	12.7	6632	1 UN89_CABEL	O01761 caenorhabdi
31	117	12.4	1197	1 CAM1_BRARE	Q90478 brachydanio
32	116.5	12.3	978	1 KFW5_RAT	Q00495 rattus norv
33	116	12.2	1240	1 NFAS_HUMAN	O94856 homo sapien

ALIGNMENTS

RESULT 1

ID	FCEA_HUMAN	STANDARD;	PRT;	257 AA.
AC	P12319			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	High affinity immunoglobulin epsilon receptor alpha-subunit precursor (FCERI) (Ige Fc receptor, alpha-subunit) (Fc-epsilon RI-alpha).			
DE	FCERI1 OR FCE1A.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88233953; PubMed=2967464;			
RA	Kochan J., Pettine L.F., Hakimi J., Kishi K., Kinet J.-P.;			
RT	"Isolation of the gene coding for the alpha subunit of the human high affinity Ige receptor.";			
RT	Nucleic Acids Res. 16:3584-3584(1988).			
RL	[2]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE= Mast cells;			
RX	MEDLINE=88158102; PubMed=2964640;			
RA	Shimizu A., Tepler J., Benfey P.N., Siraganian R.P., Leder P.;			
RT	"Human and rat mast cell high-affinity immunoglobulin E receptors: characterization of putative alpha-chain gene products.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).			
RN	[3]			
RP	3D-STRUCTURE MODELING OF 26-197			
RX	MEDLINE=93113350; PubMed=1472946;			
RA	Padlan E.A., Helm B.A.;			
RT	"A modeling study of the alpha-subunit of human high-affinity receptor for immunoglobulin-E.";			
RL	Receptor 2:129-144(1992).			
CC	-!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE) RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR . ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.			
CC	-!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO DISULFIDE LINKED GAMMA CHAINS.			
CC	-!- SUBCELLULAR LOCATION: Type 1 membrane protein.			
CC	-!- SIMILARITY: Contains 2 immunoglobulin-like domains.			
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Q05793	mus musculu
P20273	homo sapien
P09581	mus musculu
P06731	homo sapien
Q15394	homo sapien
Q810U3	rattus norv
P97685	rattus norv
Q12860	homo sapien
P12960	mus musculu
P35329	mus musculu
Q08340	macaca neme

34	115	12.2	3707	1	PGBM_MOUSE
35	115.5	12.2	847	1	CD22_HUMAN
36	115.5	12.2	977	1	KFMS_MOUSE
37	115	12.1	702	1	CEAS_HUMAN
38	114.5	12.1	837	1	NCM2_HUMAN
39	113.5	12.0	1021	1	CONT_RAT
40	113	11.9	1240	1	NFAS_MOUSE
41	113	11.9	1240	1	NFAS_RAT
42	112.5	11.9	1018	1	CONT_HUMAN
43	112.5	11.9	1020	1	CONT_MOUSE
44	110.5	11.7	862	1	CD22_MOUSE
45	110	11.6	458	1	CD4_MACNE

EMBL; X06948; CAA30025.1; -.  
 DR EMBL; J03605; AAA36204.1; -.  
 DR EMBL; A21606; CAA01564.1; -.  
 DR PIR; S00682; S00682.  
 DR PDB; IALS; 27-FEB-95.  
 DR PDB; IALT; 27-FEB-95.  
 DR PDB; 1P2Q; 08-JUN-00.  
 DR PDB; 1J86; 29-AUG-01.  
 DR PDB; 1J87; 29-AUG-01.  
 DR PDB; 1J88; 29-AUG-01.  
 DR PDB; 1J89; 05-SEP-01.  
 DR PDB; 1J89; 05-SEP-01.  
 DR Genew; HGNC:3609; FCER1A.  
 DR MIM; 147140; -.  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR InterPro; IPR007110; Ig-Like.  
 DR InterPro; IPR003598; Ig\_c2.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00408; IGC2; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; Repeat; 3D-structure.  
 FT SIGNAL 1 25  
 FT CHAIN 26 257  
 FT DOMAIN 26 205  
 FT TRANSMEM 206 224  
 FT DOMAIN 225 257  
 FT DOMAIN 30 110  
 FT DOMAIN 111 193  
 FT DISULFID 51 93  
 FT DISULFID 132 176  
 FT CARBOHYD 46 46  
 FT CARBOHYD 67 67  
 FT CARBOHYD 75 75  
 FT CARBOHYD 99 99  
 FT CARBOHYD 160 160  
 FT CARBOHYD 165 165  
 FT CARBOHYD 191 191  
 FT STRAND 31 35  
 FT HELIX 39 42  
 FT TURN 43 43  
 FT STRAND 48 54  
 FT STRAND 61 66  
 FT TURN 67 68  
 FT STRAND 69 71  
 FT STRAND 74 74  
 FT TURN 75 76  
 FT STRAND 77 79  
 FT STRAND 82 87  
 FT HELIX 91 96  
 FT TURN 98 100  
 FT TURN 101 101  
 FT STRAND 104 107  
 FT STRAND 114 116  
 FT HELIX 120 124  
 FT STRAND 128 133  
 FT STRAND 143 145  
 FT STRAND 146 148  
 FT TURN 149 149  
 FT STRAND 150 150  
 FT TURN 152 153  
 FT STRAND 154 155  
 FT TURN 156 159  
 FT STRAND 160 163  
 FT HELIX 165 170  
 FT STRAND 175 178  
 FT STRAND 181 182  
 FT TURN 183 185  
 FT STRAND 186 187  
 FT STRAND 190 193  
 SQ SEQUENCE 257 AA; 29596 MW; F183BB2357DDAD58 CRC64;  
 100.0%; Score 947; DB 1; Length 257;

Best Local Similarity 100.0%; Pred. No. 5,8e-77;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VPQPKVSLNPPNRIKGENVTLCNGNNPFEVSTKWFHNGSLSEETNSLNIIVNAKF 60  
 DB 26 VPQPKVSLNPPNRIKGENVTLCNGNNPFEVSTKWFHNGSLSEETNSLNIIVNAKF 85  
 QY 61 EDSEGYKCOHQVNESEPVYLVFSDWLLQSAEVMWEGQPLFLRCHGRWMDVYKVIY 120  
 DB 86 EDSEGYKCOHQVNESEPVYLVFSDWLLQSAEVMWEGQPLFLRCHGRWMDVYKVIY 145  
 QY 121 YKDGKALKYENHNISITNATVEDSGTYCTGKVMQLDYSEPLNITVIKA 172  
 DB 146 YKDGKALKYENHNISITNATVEDSGTYCTGKVMQLDYSEPLNITVIKA 197  
 RESULT 2  
 FCEA\_MOUSE  
 ID FCEA\_MOUSE STANDARD; PRT; 250 AA.  
 AC P20489;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor  
 DE (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).  
 GN FCER1A OR FCE1A.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89359361; PubMed=2527850;  
 RA Ra C., Jouvin M.H.E., Kinet J.-P.;  
 RT "Complete structure of the mouse mast cell receptor for IgE (Fc  
 epsilon RI) and surface expression of chimeric receptors  
 (rat-mouse-human) on transfected cells.";  
 RL J. Biol. Chem. 264:15323-15327(1989).  
 CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH  
 CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC  
 CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL  
 CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)  
 CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR  
 CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.  
 CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO  
 CC DISULFIDE LINKED GAMMA CHAINS.  
 CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.  
 CC  
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 CC  
 CC EMBL; J05018; AAA37600.1; -.  
 CC FIR; A34342; A34342.  
 CC HSP; P12319; IALS.  
 CC MGI; 95494; Fcer1a.  
 CC GO; GO:0007165; P:signal transduction; IDA.  
 CC InterPro; IPR007110; Ig-Like.  
 CC InterPro; IPR003599; Ig.  
 CC Pfam; PF00047; Ig; 2.  
 CC SMART; SM00409; Ig; 2.  
 CC PROSITE; PS50835; IG\_LIKE; 1.  
 KW IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; Repeat.  
 FT SIGNAL 1 23  
 FT CHAIN 24 250  
 FT DOMAIN 24 204  
 FT HIGH AFFINITY IMMUNOGLOBULIN EPSILON  
 FT RECEPTOR ALPHA-SUBUNIT.  
 FT EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 205 223 POTENTIAL.
FT DOMAIN 224 250 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 104 IG-LIKE 1.
FT DOMAIN 114 181 IG-LIKE 2.
FT DISULFID 49 92 BY SIMILARITY.
FT DISULFID 131 174 BY SIMILARITY.
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 250 AA; 28672 MW; 2575D1BF84DC0C4E CRC64;

Query Match 49.8%; Score 472; DB 1; Length 250;
Best Local Similarity 51.5%; Pred. No. 7.4e-35;
Matches 88; Conservative 35; Mismatches 46; Indels 2; Gaps 2;

QY 3 QPKVSLNPPNRIKFGENTVLTGNNFFEV-SSTKWFHNGSLSEETNSLNIIVNAKFE 61
DB 26 EKSVTLDPFWIRIFTGKVTLSGVNHLQSNSTTKWIHNGTVSEVNSHLVIVSATVQ 85

QY 62 DSGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVMEGQPLFLRCHGWRNWDVYKVIY 121
DB 86 DSGYICQKQGLFKSKPYLVNTQDWLLQLQASAEVMEGQPLFLRCHGWRNWDVYKVIY 145

QY 122 KDGEALKYWEHNHISITNAVDSGTYYCTGKVAQLDYSEPLNITVIKA 172
DB 146 RNDHAFNYSYES-PVSIREATLNDSGTVHCKGYLRQVEYSDFKRIAVVKA 195

RESULT 3
FCBL RAT STANDARD; PRT; 245 AA.
AC P12371;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
GN FCER1A OR FCE1A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN [2]
RX MEDLINE=88024987; PubMed=2959318;
RA Kinet J.-P., Metzger H., Hakini J., Kochan J.;
RT "A cDNA presumptively coding for the alpha subunit of the receptor.
RT with high affinity for immunoglobulin E.";
RL Biochemistry 26:4605-4610(1987).
RP REVISIONS.
RA Kochan J.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Mast cells;
RX MEDLINE=88159102; PubMed=2964640;
RA Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,
RA Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).
RN [4]
RP SEQUENCE OP 21-245 FROM N.A.
RX MEDLINE=88289772; PubMed=2969594;
RA Liu F.-T., Albrandt K., Robertson M.W.;
RT "cDNA heterogeneity suggests structural variants related to the high-
RT affinity IGE receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643(1988).
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH

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CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
CC DISULFIDE LINKED GAMMA CHAINS.
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M17153; AAA42045.1; -
CC EMBL; J03606; AAA41582.1; -
CC EMBL; M21622; AAA41146.1; -
CC PIR; C31327; A30154.
CC HSSP; P12319; IALS.
CC InterPro; IPR007110; IG-Like.
CC InterPro; IPR003599; IG.
CC Pfam; P20047; Ig; 2.
CC SMART; SM00409; IG; 2.
CC PROSITE; PS50835; IG LIKE; 1.
CC IGE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 245 HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT RECEPTOR ALPHA-SUBUNIT.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE 1.
FT IG-LIKE 2.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 245 AA; 27793 MW; A0B67DD363B72197 CRC64;

Query Match 49.4%; Score 468; DB 1; Length 245;
Best Local Similarity 50.9%; Pred. No. 1.6e-34;
Matches 86; Conservative 33; Mismatches 50; Indels 0; Gaps 0;

QY 3 QPKVSLNPPNRIKFGENTVLTGNNFFEVSTKWFHNGSLSEETNSLNIIVNAKFD 62
DB 26 QKSVSLDPPWIRILTQGVTLICGNNSSQMMSTKWIHNDISNVKSHWIVSATIQD 85

QY 63 SGGEYKCOHQVNESEPVYLEVFSDWLLQLQASAEVMEGQPLFLRCHGWRNWDVYKVIY 122
DB 86 SGYICQKQGYKSKPYLVNMQEWLLQLQASAEVMEGQPLFLRCHGWRNWDVYKVIY 145

QY 123 DGEALKYWEHNHISITNAVDSGTYYCTGKVAQLDYSEPLNITVIK 171
DB 146 DDIAFKYSYDSNNISIRKATFNDSGSHCTGYLNKVECKSKFSAVVK 194

RESULT 4
FCG2_BOVIN
ID FCG2_BOVIN STANDARD; PRT; 296 AA.
AC Q28110;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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KW Immunoglobulin domain; Repeat; Alternative splicing; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 374
FT
FT HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC
FT RECEPTOR I.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT IG-LIKE C2-TYPE 3.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT HEKVTSTSIQDRHLEELKQKQEEQJQEGVHRKEPOGA
FT T -> QCALEAPTQGA (in isoform B).
FT /FTid=VSP_002637.
FT L -> T.
FT /FTid=VAR_003953.
FT N -> V.
FT /FTid=VAR_003954.
FT S -> T (IN REF. 1; CAA32536).
FT CONFLICT 25 25
FT SEQUENCE 374 AA; 42605 MW; 2C2AA8103ECF16E6 CRC64;

Query Match 39.5%; Score 374.5; DB 1; Length 374;
Best Local Similarity 41.6%; Pred. No. 5.4e-26;
Matches 69; Conservative 36; Mismatches 60; Indels 1; Gaps 1;

QY 4 KPKVSLNPPWNRIFKGNVTLTCGNFFVSVSTKWFHNGSLSEETNSLINVNAKPEDS 63
D 21 KAVISLQPPWVSIFQKENVTLWCCEGPHLPQDSSTQWFLNGTATQTSTPSYRITSASVND 80
QY 64 GEYKCOHQVNESEPVYLEVFSWLLQLQASAEVWMEQPLFLRCHGWNDVYKYYKD 123
D 81 GEYRCQGLSGRSDPIQLQHRGWLQLQVSRVFTGEPEPLARCHAWKOKLVNVDYRN 140
QY 124 GEALKYWNHNISITNATVEDSGTYCTGKVMQLDYSEPLNITY 169
D 141 GKAFKPFHNSNLTKLNKSHNGTYHCSG-MGKHRYTSAGISVTV 185

RESULT 6
FCG1 MOUSE
ID_FCG1 MOUSE STANDARD; PRT; 404 AA.
AC P26151;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin gamma Fc receptor I precursor (Fc-gamma RI) (FcR1) (IgG Fc receptor I).
GN FCGR1 OR FCG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=90111035; PubMed=2136886;
RA Sears D.W., Osman N., Tate B., McKenzie I.F.C., Hogarth P.M.;
RT "Molecular cloning and expression of the mouse high affinity Fc
receptor for IgG."
RL J. Immunol. 144:371-378 (1990).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=92166399; PubMed=1531670;
RA Osman N., Korak C.A., McKenzie I.F., Hogarth P.M.;
RT "Structure and mapping of the gene encoding mouse high affinity Fc

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RT gamma RI and chromosomal location of the human Fc gamma RI gene." ;
RL J. Immunol. 148:1570-1575 (1992).
J. FUNCTION: Binds to the Fc region of immunoglobulins gamma. High
affinity receptor.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Macrophage specific.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-10 is the initiator.
CC
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CC
CC -----
CC EMBL; M31314; AAA40056.1; -.
CC PIR; A46480; A46480.
CC HSSP; P12319; 1ALS.
CC MGD; MGI:95498; Fcgr1.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00408; IGC2; 1.
CC PROSITE; PS00835; IG_LIKE; 2.
CC Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
KW SIGNAL 1 24
KW CHAIN 25 404
FT HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC
FT RECEPTOR I.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE 1.
FT IG-LIKE C2-TYPE 2.
FT IG-LIKE C2-TYPE 3.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT GEALKYWNHNISITNATVEDSGTYCTGKVMQLDYSEPLNITY 169
D 151 GKSFQF-SSDSEVALKTNLSHSGIYHCSG-TGRHRYTSAGVSIIV 194

Query Match 39.0%; Score 369; DB 1; Length 404;
Best Local Similarity 43.4%; Pred. No. 1.8e-25;
Matches 72; Conservative 35; Mismatches 57; Indels 2; Gaps 2;

QY 4 KPKVSLNPPWNRIFKGNVTLTCGNFFVSVSTKWFHNGSLSEETNSLINVNAKPEDS 63
D 31 KAVITLQPPWVSIFQKENVTLWCCEGPHLPQDSSTQWFLNGTAVQISTPSYIPEASFQDS 90
QY 64 GEYKCOHQVNESEPVYLEVFSWLLQLQASAEVWMEQPLFLRCHGWNDVYKYYKD 123
D 91 GEYRCQIGSSMPSPDVLQIHNWLLQASRRVLTEGEPEPLARCHGWKNKLVNVDYRN 150
QY 124 GEALKYWNHNISITNATVEDSGTYCTGKVMQLDYSEPLNITY 169
D 151 GKSFQF-SSDSEVALKTNLSHSGIYHCSG-TGRHRYTSAGVSIIV 194

RESULT 7
FCG3 BOVIN
ID_FCG3 BOVIN STANDARD; PRT; 250 AA.
AC P79107;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III precursor
(IgG Fc receptor III) (Fc-gamma RIII) (FcRIII).

```

GN FCGR3 OR FCGR11.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph node;  
 RX MEDLINE=97246739; PubMed=9089104;  
 RA Collins R.A., Gelder K.I., Howard C.J.;  
 RT "Nucleotide sequence of cattle FCGR11: its identification in  
 RT gammadelta T cells";  
 RL Immunogenetics 45:440-443(1997).  
 CC -!- FUNCTION: IS A RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED  
 CC OR AGGREGATED IGG AND ALSO MONOMERIC IGG. ALSO MEDIATES ANTIBODY-  
 CC DEPENDENT CELLULAR TOXICITY (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN GAMMA-DELTA T CELLS.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -!- CAUTION: IT IS NOT SURE IF THE VARIANTS ARE DUE TO DIFFERENT  
 CC ALLELES OR TO THE EXISTENCE OF AT LEAST TWO GENES.  
 CC -----  
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 CC -----  
 DR EMBL; X9595; CAA68026.1; -.  
 DR HSP; F12319; IALUS.  
 DR InterPro; IPR007110; Ig-like.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 KW IGG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; Repeat; Polymorphism.  
 FT SIGNAL 1 16  
 FT CHAIN 17 250  
 FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC  
 FT REGION RECEPTOR III.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT DOMAIN 17 208  
 FT TRANSMEM 209 225  
 FT DOMAIN 226 250  
 FT CHAIN 23 105  
 FT DOMAIN 99 189  
 FT DISULFID 47 89  
 FT DISULFID 128 172  
 FT CARBOHYD 56 56  
 FT CARBOHYD 63 63  
 FT CARBOHYD 180 180  
 FT VARIANT 11 11  
 FT VARIANT 12 12  
 FT VARIANT 46 46  
 FT VARIANT 107 107  
 FT VARIANT 114 114  
 FT VARIANT 229 229  
 FT VARIANT V -> I.  
 SQ SEQUENCE 250 AA; D5625139E889E207 CRC64;  
 Query Match 38.5%; Score 365; DB 1; Length 250;  
 Best Local Similarity 42.9%; Pred. No. 2.3e-25;  
 Matches 72; Conservative 26; Mismatches 70; Indels 0; Gaps 0;  
 QY 2 POKPKVSLNPNWRIKFGENVTLTCNGNFFVSSSTKWFHNGSLSEETNSLINVAKFE 61  
 DB 23 PSKAVLLDQWHLVLTNDVTLKQGDYDPVENSFKWHTGLTSSQTFSPFYADVQVQ 82  
 QY 62 DSGYKCKQHQVNSEPVLVEFSDWLLQASAEVMEGQPLFRCGRNWDVYKVIY 121  
 DB 83 DSGEYKQQTGLSPADPKLVKLEHVHVMGLLQVAVRNVGVKPIRLKCHSWKTKTFAVQVYF 142  
 QY 122 KDGEALKYVYENHNSITNATVEDSGTYCTGKQWQLDYSEPLNTV 169

Db 143 RNRGKGYSHGNSDFHPEAKLEHSGYFCRGLIGKNSSBSVOITV 190  
 RESULT 8  
 FCGR2\_CAVPO STANDARD; PRT; 341 AA.  
 ID FCG2\_CAVPO Q60513; Q60498; Q60511; Q60512;  
 AC Q60513; Q60498; Q60511; Q60512;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-  
 DE gamma RII) (FCRII) (IgG Fc receptor II) (Fc-gamma-1/gamma-2 receptor).  
 GN FCGR2.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2R-B1).  
 RX MEDLINE=90241239; PubMed=1692213;  
 RA Tomimaga M., Sakata A., Ohmura T., Yamashita T., Koyama J., Onoue K.;  
 RT "The structure and expression of the guinea pig Fc receptor for IgG1  
 RT and IgG2 (Fc gamma 1/gamma 2R).";  
 RL Biochem. Biophys. Res. Commun. 168:683-689(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 2R-B1; 2R-B2 AND 2R-B3).  
 RC STRAIN=JY-1;  
 RX MEDLINE=93346746; PubMed=8345193;  
 RA Yamashita T., Shinohara K., Yamashita Y.;  
 RT "Expression Cloning of complementary DNA encoding three distinct  
 RT isoforms of guinea pig Fc receptor for IgG1 and IgG2.";  
 RL J. Immunol. 151:2014-2023(1993).  
 CC -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low  
 CC affinity receptor.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Name=2R-B3; Sequence=VSP\_002639;  
 CC Name=2R-B1;  
 CC Name=2R-B2;  
 CC Name=2R-B3; Sequence=VSP\_002638;  
 CC TISSUE SPECIFICITY: Macrophages and polymorphonuclear leukocytes  
 CC express preferentially isoform 2R-B1. B lymphocytes express  
 CC isoform 2R-B1, isoform 2R-B2 and isoform 2R-B3.  
 CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred  
 CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).  
 CC This motif is involved in downmodulation of cellular responses.  
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
 CC -----  
 DR EMBL; D13693; BAA02852.1; -.  
 DR EMBL; D13692; BAA02851.1; -.  
 DR EMBL; D13691; BAA02850.1; -.  
 DR EMBL; M35272; AAA37036.1; ALT\_INIT.  
 DR HSP; P12319; IALUS.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 2.  
 DR PROSITE; PS50835; IG LIKE; 2.  
 KW IGG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 KW Immunoglobulin domain; Repeat; Alternative splicing.  
 FT SIGNAL 1 42  
 FT CHAIN 43 341  
 FT LOW AFFINITY IMMUNOGLOBULIN GAMMA FC  
 FT REGION RECEPTOR II.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 43 224

FT TRANSMEM 225 245 POTENTIAL  
FT DOMAIN 246 341 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 48 125 IG-LIKE C2-TYPE 1.  
FT DOMAIN 131 213 IG-LIKE C2-TYPE 2.  
FT SITE 318 323 ITIM MOTIF.  
FT DISULFID 71 113 BY SIMILARITY.  
FT DISULFID 152 196 BY SIMILARITY.  
FT CARBOHYD 73 79 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 180 180 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 187 187 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 195 195 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT VARSPLIC 273 301 GEYSVFGGMMSCPGDGLPDPARTDLS -> A (in isoform 2R-B2).  
FT FT /FTIG-VSP 002638.  
FT FT GNPEHREMGETIPEDGEYSVFGGMMSCPGDGLPDPAR  
FT FT TDLS -> A (in isoform 2R-B1).  
FT FT /FTIG-VSP 002639.  
FT FT Q -> QVLPYSYRFTAKGNDSGEYRQ (IN REF. 1).  
FT CONFLICT 114 114  
FT SEQUENCE 341 AA; 37091 MW; 5137E3271D43B84 CRC64;  
Query Match 38.3%; Score 363; DB 1; Length 341;  
Best Local Similarity 43.3%; Pred. No. 5e-25;  
Matches 73; Conservative 21; Mismatches 74; Indels 0; Gaps 0;  
QY 2 POKPKVSLNPPNRIKFGENVILTCGNPNFFSVSTKFWHNGSLSEETNSLNINNAKPE 61  
Db 47 PPKAVVLEPPVQLVGRDRLTLCGAPSGNHSTQWLHNGSLIPTQVLPSYRFTAKGN 106  
QY 62 DSEYKQCOQVNEPVLVEFSDMLLQASVVMWEGQPLFLRGHWNVDVKVYV 121  
Db 107 DSEYKQCGAGTSLSDPFLVDVLSLQVLFQEGDGVILRCHSWNNWPLAKVTFY 166  
QY 122 KDGEALKYVYENHISITNATVEDSGTYCTGKWQWLDYSEPLNITV 169  
Db 167 HNGVAKYFISIKNFIPOAHSHSGAYNCTGLIGTSHTSPPTIV 214  
RESULT 9  
FC3A\_HUMAN  
ID FC3A\_HUMAN STANDARD; PRT; 254 AA.  
AC P08637; 1998 (Rel. 08, Created)  
DT 01-AUG-1998 (Rel. 15, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Low affinity immunoglobulin gamma Fc region receptor III-A precursor  
DE (IgG Fc receptor III-2) (Fc-gamma RIIII) (Fc-gamma RIIIA)  
DE (FCRIIA) (Fc-gamma RIIII) (FCRII) (CD16-A) (FCR-10).  
DE FCR3A OR FCG3 OR FCGR3 OR IGR3 OR CD16A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89328325; PubMed=2526846;  
RA Ravetch J.V., Perussia B.;  
RT "Alternative membrane forms of Fc gamma RIIII (CD16) on human natural killer cells and neutrophils. Cell type-specific expression of two genes that differ in single nucleotide substitutions.";  
RL J. Exp. Med. 170:481-497 (1989).  
RN [2]  
RP SEQUENCE OF 1-39 FROM N.A.  
RX MEDLINE=95138131; PubMed=7836402;  
RA Gessner J.E., Grussemeyer T., Kolanus W., Schmidt R.E.;  
RT "The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Molecular characterization of the promoter regions.";  
RL J. Biol. Chem. 270:1350-1356 (1995).  
RN [3]  
RP VARIANTS ARG-66 AND HIS-66.  
RX MEDLINE=96183251; PubMed=8609432;  
RA de Haas M., Koene H.R., Kleijer M., de Vries E., Simsek S.,

van Tol M.J.D., Roos D., von dem Borne A.E.G.K.;  
RT "A triallelic Fc gamma receptor type IIIA polymorphism influences the binding of human IgG by NK cell Fc gamma RIIIA.";  
RL J. Immunol. 156:3948-3955 (1996).  
RN [4]  
RP VARIANT VAL-157.  
RX MEDLINE=97385047; PubMed=9242542;  
RA Koene H.R., Kleijer M., Algra J., Roos D., von dem Borne A.E.G.K., de Haas M.;  
RT "Fc gamma RIIIA-158V/F polymorphism influences the binding of IgG by natural killer cell Fc gamma RIIIA, independently of the Fc gamma RIIIA-48L/R/H phenotype.";  
RL Blood 90:1109-1114 (1997).  
RN [5]  
RP VARIANT VAL-176.  
RX MEDLINE=97426467; PubMed=9276722;  
RA Wu J., Ederberg J.C., Redecha P.B., Bansal V., Guyre P.M., Coleman K., Salmon J.E., Kimberly R.P.;  
RT "A novel polymorphism of Fc gamma RIIIA (CD16) alters receptor function and predisposes to autoimmune disease.";  
RL J. Clin. Invest. 100:1059-1070 (1997).  
CC -!- FUNCTION: RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED OR AGGREGATED IGG AND ALSO MONOMERIC IGG. MEDIATES ANTIBODY-DEPENDENT CELLULAR CYTOTOXICITY (ADCC) AND OTHER ANTIBODY-DEPENDENT RESPONSES, SUCH AS PHAGOCYTOSIS.  
CC -!- SUBUNIT: EXISTS AS A HETERO-OLIGOMERIC RECEPTOR COMPLEX WITH FC EPSILON RECEPTOR I GAMMA SUBUNIT AND / OR THE CD3 ZETA SUBUNIT.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Exists also as a soluble receptor.  
CC -!- TISSUE SPECIFICITY: Expressed on natural killer cells, macrophages, subpopulation of T cells, immature thymocytes and placental trophoblasts.  
CC -!- PTM: Glycosylated. Contains high mannose- and complex-type oligosaccharides.  
CC -!- PTM: The soluble form is produced by a proteolytic cleavage.  
CC -!- POLYMORPHISM: Isoform Val-157 shows a higher binding capacity of IGG1, IGG3 and IGG4 compared with isoform Phe-157. Alleles Leu-66 and Phe-157, and alleles His-66 / Arg-66 and Val-157 are in linkage disequilibrium.  
CC -!- MISCELLANEOUS: ENCODED BY ONE OF TWO NEARLY IDENTICAL GENES: FCGR3A (SHOWN HERE) AND FCGR3B WHICH ARE EXPRESSED IN A TISSUE-SPECIFIC MANNER. THE PHE-203 IN III-A DETERMINES THE TRANSMEMBRANE DOMAINS WHEREAS THE SER-203 IN III-B DETERMINES THE GPI-ANCHORING.  
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD16A entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd16a.htm".  
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CC EMBL; X52645; CAA36870.1; -;  
CC EMBL; Z46222; CAA86295.1; -;  
CC PIR; JLO107; JLO107.  
CC HSP; P12319; IALS.  
CC Genew; HGNC:3619; FCGR3A.  
CC MIM; 146740; -;  
CC GO; GO:0005886; C:plasma membrane; TAS.  
CC GO; GO:0006955; P:immune response; TAS.  
CC InterPro; IPR007110; IG-like.  
CC InterPro; IPR003599; IG.  
CC Pfam; PF00447; ig; 2.  
CC SMART; SM00409; IG; 2.  
CC PROSITE; PS50835; IG\_LIKE; 2.  
KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain; Repeat; Multigene family; Polymorphism.  
RN SIGNAL 1 16  
RN CHAIN 17 254  
RN REGION RECEPTOR III-A.



```

RT "Cloning and sequence of the cDNA coding for rat type II Fc gamma
RT receptor of mast cells.";
RL FEBS Lett. 331:86-90(1993).
CC !- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low
CC affinity receptor. By binding to IgG it initiates cellular
CC responses against pathogens and soluble antigens.
CC !- SUBCELLULAR LOCATION: Type I membrane protein.
CC !- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in downmodulation of cellular responses.
CC The phosphorylated ITIM motif binds to the SH2 domain of
CC PTPN6/SHP-1.
CC !- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC -----
DR EMBL; X73371; CAA51788.1; -.
DR PIR; S36903; S36903.
DR HSSP; P12319; IALS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 31
FT CHAIN 32 285
FT DOMAIN 32 212 LOW AFFINITY IMMUNOGLOBULIN GAMMA Fc
FT TRANSMEM 213 233 REGION RECEPTOR II
FT DOMAIN 234 285 EXTRACELLULAR (POTENTIAL).
FT POTN6 36 118 POTENTIAL.
FT DOMAIN 119 201 CYTOPLASMIC (POTENTIAL).
FT SITE 262 267 IG-LIKE C2-TYPE 1.
FT SITE 262 267 IG-LIKE C2-TYPE 2.
FT DISULFID 59 101 ITIM MOTIF.
FT DISULFID 140 184 BY SIMILARITY.
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 94 94 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SSSEQUENCE 285 AA; 32047 MW; 255540A584CFFA0A CRC64;
Query Match 37.8%; Score 358; DB 1; Length 285;
Best Local Similarity 40.4%; Pred. No. 1.1e-24;
Matches 67; Conservative 33; Mismatches 66; Indels 0; Gaps 0;
QY 4 KPVKSLNPPNRIKGNVTILTCGNFFVSTKWHNGSLSEETNSSINIVNAKPEDS 63
DB 37 KAVVLEPPWIOVLKEDTVTLMCEGTHNTKNCSTQWFHNGSSIWHOQAQNYTFKATVND 96
QY 64 GEYKCOHQVNESEPVVLEVFSDWLLLOASAEVVMGQPLFLRCHGWRNWDVVKVYKXD 123
DB 97 GEVRCRMEETGISEPHLGVISDWLLLOTSQLVFEGETITLCHSKWKQLTKVLLFQN 156
QY 124 GEALKVYKHNNISITNATVEDSGTYCTGKWKQWLDYSEPLNIV 169
DB 157 GKPVRYVYHQSNFISIPKXNHSNGNYCKAVLGRVTWHSKPVITV 202
RESULT 12
FC3B HUMAN
ID FC3B HUMAN STANDARD; PRT; 233 AA.
AC O75015;
DT 30-MAY-2000 (Rel. 39, Created)

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DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAY-2004 (Rel. 43, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III-B precursor
DE (IgG Fc receptor III-1) (Fc-gamma RIII-beta) (Fc-gamma RIIIB)
DE (FCRIIB) (Fc-gamma RIII) (FCRII) (CD16-B) (FCR-10).
DE FCR3B OR FC3 OR FCR3 OR IGR3 OR CD16B.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (VARIANT NA-2).
RX MEDLINE=89328325; PubMed=2526846;
RA Ravetch J.V., Perussia B.;
RT "Alternative membrane forms of Fc gamma RIII(CD16) on human natural
RT killer cells and neutrophils. Cell type-specific expression of two
RT genes that differ in single nucleotide substitutions.";
RL J. Exp. Med. 170:481-497(1989).
RN [2]
RP SEQUENCE FROM N.A. (VARIANT NA-2).
RX TISSUE=Placenta;
RA MEDLINE=88232937; PubMed=2967436;
RA Simmons D., Seed B.;
RT "The Fc gamma receptor of natural killer cells is a phospholipid-
RT linked membrane protein.";
RL Nature 333:568-570(1988).
RN [3]
RP ERRATUM.
RA Simmons D., Seed B.;
RL Nature 340:662-662(1989).
RN [4]
RP SEQUENCE FROM N.A. (VARIANT NA-1).
RX TISSUE=Leukocyte;
RA MEDLINE=89128838; PubMed=2521732;
RA Peltz G.A., Grundy H.O., Lebo R.V., Yssel H., Barsh G.S., Moore K.W.;
RT "Human Fc-gamma-RIII: Cloning, expression, and identification of the
RT chromosomal locus of two Fc receptors for IgG.";
RN Proc. Natl. Acad. Sci. U.S.A. 86:1013-1017(1989).
RN [5]
RP SEQUENCE OF 1-72 FROM N.A. (VARIANT NA-2).
RX TISSUE=Placenta;
RA MEDLINE=95138131; PubMed=7836402;
RA Gesener J.E., Grussemeyer T., Kolanus W., Schmidt R.E.;
RT "The human low affinity immunoglobulin G Fc receptor III-A and III-B
RT genes. Molecular characterization of the promoter regions.";
RN J. Biol. Chem. 270:1350-1361(1995).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) IN COMPLEX WITH IGG1 Fc.
RX MEDLINE=20372189; PubMed=10917521;
RA Sonderrmann P., Huber R., Oosthuizen V., Jacob U.;
RT "The 3.2-A crystal structure of the human IGG1 Fc fragment-Fc
RT gammaRIII complex.";
RL Nature 406:267-273(2000).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 19-192.
RX MEDLINE=20471519; PubMed=11021536;
RA Zhang Y., Boesen C.C., Radaev S., Brooks A.G., Fridman W.H.,
RA Sautes-Fridman C., Sun P.D.;
RT "Crystal structure of the extracellular domain of a human Fc gamma
RT RIII.";
RL Immunity 13:387-395(2000).
RN [8]
RP VARIANT SH ASP-78.
RX MEDLINE=97180159; PubMed=9028335;
RA Bux J., Stein E.L., Bierling P., Fromont P., Clay M., Stroncek D.,
RA Santoso S.;
RT "Characterization of a new alloantigen (SH) on the human neutrophil Fc
RT gamma receptor IIIB.";
RL Blood 89:1027-1034(1997).
CC !- FUNCTION: RECEPTOR FOR THE Fc REGION OF IMMUNOGLOBULINS GAMMA. LOW
CC AFFINITY RECEPTOR. BINDS COMPLEXED OR AGGREGATED IGG AND ALSO
CC MONOMERIC IGG. CONTRARY TO III-A, IS NOT CAPABLE TO MEDIATE
CC ANTIBODY-DEPENDENT CYTOTOXICITY AND PHAGOCYTOSIS. MAY SERVE AS A

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RP SEQUENCE FROM N.A. (ISOFORMS IIB1 AND IIB2).  
 RX MEDLINE=91079576; PubMed=1824594;  
 RA Hogarth P.M., Witort E., Hulet M.D., Bonnerot C., Even J.,  
 RA Fridman W.H., McKenzie I.F.C.;  
 RT "Structure of the mouse beta Fc gamma receptor II gene.";  
 RL J. Immunol. 146:369-376(1991).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM IIB1').  
 RN STRAIN=DBA/2; TISSUE=Mast cells;  
 RX MEDLINE=96264690; PubMed=8683114;  
 RA Latour S., Fridman W.H., Daeron M.;  
 RT "Identification, molecular cloning, biologic properties, and tissue  
 RT distribution of a novel isoform of murine low-affinity Igg receptor  
 RT homologous to human Fc gamma RIIb1.";  
 RL J. Immunol. 157:189-197(1996).  
 RN [7]  
 RP SEQUENCE OF 30-330 FROM N.A. (ISOFORMS IIB1 AND IIB2).  
 RC STRAIN=DBA/2, and NZB; TISSUE=Spleen;  
 RX MEDLINE=96128267; PubMed=8537115;  
 RA Sawchuk D.J., Mahmood M., Cairns E., Sinclair N.R.S.;  
 RT "Nonsynonymous mutations in an Fc-receptor structural gene in NZB  
 RT mice.";  
 RL Immunogenetics 43:112-113(1995).  
 RN [8]  
 RP SEQUENCE OF 17-45 FROM N.A.  
 RX MEDLINE=96313694; PubMed=2944118;  
 RA Hibbs M.L., Walker I.D., Kirszenbaum L., Peitersz G.A., Deacon N.J.,  
 RA Chambers G.W., McKenzie I.F.C., Hogarth P.M.;  
 RT "The murine Fc receptor for immunoglobulin: purification, partial  
 RT amino acid sequence, and isolation of cDNA clones."  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6980-6984(1986).  
 RN [9]  
 RP CHARACTERIZATION OF ISOFORM IIB3.  
 RC TISSUE=Macrophage;  
 RX MEDLINE=94001803; PubMed=8398981;  
 RA Tartour E., de la Salle H., de la Salle C., Teillaud C., Camoin L.,  
 RA Galinha A., Latour S., Hanau D., Fridman W.H., Sautes C.;  
 RT "Identification, in mouse macrophages and in serum, of a soluble  
 RT receptor for the Fc portion of IgG (Fc gamma R) encoded by an  
 RT alternatively spliced transcript of the Fc gamma RII gene.";  
 RL Int. Immunol. 5:859-868(1993).  
 RN [10]  
 RP FUNCTION: Receptor for the Fc region of complexed immunoglobulins  
 gamma. Low affinity receptor. Involved in a variety of effector  
 and regulatory functions such as phagocytosis of antigen-antibody  
 complexes from the circulation and modulation of antibody  
 production by B-cells. Isoform IIB1 and isoform IIB1' form caps  
 but fail to mediate endocytosis or phagocytosis. Isoform IIB2 can  
 mediate the endocytosis of soluble immune complexes via clathrin-  
 coated pits. Isoform IIB1 and isoform IIB2 can downregulate B-  
 cell, T-cell, and mast cell activation when coaggregated to B-cell  
 receptors for AG (BCR), T-cell receptors for AG (TCR), and Fc  
 receptors, respectively.  
 CC -! SUBCELLULAR LOCATION: Type I  
 CC membrane protein. Isoform IIB1 binds the cytoskeleton and is not  
 CC localised in endocytotic pits. Isoform IIB3 is released as a  
 CC soluble molecule.  
 CC -! ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=IIB3; Synonyms=Beta-1;  
 CC IsoId=P08101-1; Sequence=Displayed;  
 CC Name=IIB2; Synonyms=Beta-2;  
 CC IsoId=P08101-2; Sequence=VSP\_002640;  
 CC Name=IIB1'; Synonyms=Beta-1';  
 CC IsoId=P08101-3; Sequence=VSP\_002641;  
 CC Name=IIB3; Synonyms=Beta-3;  
 CC IsoId=P08101-4; Sequence=Not described;  
 CC -! TISSUE SPECIFICITY: Widely expressed by cells of hemopoietic  
 CC origin. The isoforms are differentially expressed. Isoform IIB1 is  
 CC preferentially expressed by cells of the lymphoid lineage, isoform  
 CC IIB2 by cells of the myeloid lineage, and isoform IIB3 is released  
 CC by macrophages and is present in the serum. Isoform IIB1' is  
 CC expressed in myeloid and lymphoid cell lines, in normal spleen  
 CC cells, and in resting or LPS-activated B-cells but is not detected

CC in mesenteric lymph node cells.  
 CC -! DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred to  
 CC as the Immunoreceptor tyrosine-based inhibitor motif (ITIM). This  
 CC motif is involved in downmodulation of cellular responses. The  
 CC phosphorylated ITIM motif binds to the SH2 domain of PTPN6/SHP-1.  
 CC Another tyrosine-containing sequence, more C-terminal, accounts  
 CC for the ability of isoform IIB2 to trigger the phagocytosis of  
 CC particulate immuno complexes.  
 CC -! PTM: Glycosylated.  
 CC -! PTM: When coaggregated to BCR, isoform IIB1 and isoform IIB1'  
 CC become tyrosine phosphorylated and bind to the SH2 domains of  
 CC the protein tyrosine phosphatase PTPN6.  
 CC -! POLYMORPHISM: Ly-17, alloantigenic system involves residues 116 and  
 CC 161. Ly-17.1 mice are Pro-116 and Glu-161; Ly-17.2 mice are Leu-  
 CC 116 and Leu-161. These polymorphisms do not affect IGG binding.  
 CC -! SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M16367; AAA37608.1; -  
 CC EMBL; M14216; AAA37609.1; -  
 CC EMBL; M17515; AAA37607.1; -  
 CC EMBL; N31312; AAA37610.1; -  
 CC EMBL; X04648; CAA28309.1; ALT\_INIT.  
 CC EMBL; U31801; AAA92707.1; -  
 CC EMBL; U31802; AAA92708.1; -  
 CC EMBL; U31803; AAA92709.1; -  
 CC EMBL; U31804; AAA92710.1; -  
 CC EMBL; M14276; AAA37605.1; -  
 CC EMBL; U51629; AAA97464.1; -  
 CC PIR; B40071; FCMG1.  
 CC PIR; I49660; I49660.  
 CC GlycoSuiteDB; P08101; -  
 CC MGD; MGI:95499; Fcgr2b.  
 CC GO; GO:0003793; F:defense/immunity protein activity; IMP.  
 CC GO; GO:0006955; P:immune response; IMP.  
 CC InterPro; IPR007110; IG-like.  
 CC Pfam; PF00047; IG; 2.  
 CC PROSITE; PS50835; IG\_LIKE; 1.  
 CC Igg-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;  
 CC Immunoglobulin domain; Repeat; Alternative splicing; Phosphorylation;  
 CC Polymorphism.  
 CC SIGNAL 1 29  
 CC CHAIN 30 330  
 CC -----  
 CC DOMAIN 30 210  
 CC TRANSMEM 211 231  
 CC DOMAIN 232 330  
 CC DOMAIN 50 106  
 CC DOMAIN 131 189  
 CC SITE 307 312  
 CC DISULFID 57 99  
 CC DISULFID 138 182  
 CC CARBOHYD 65 65  
 CC CARBOHYD 92 92  
 CC CARBOHYD 166 166  
 CC CARBOHYD 173 173  
 CC VARSPLIC 243 290  
 CC -----  
 CC VARSPLIC 262 290  
 CC -----  
 CC VARIANT 116 116  
 CC VARIANT 116 116  
 CC VARIANT 145 145  
 CC -----  
 CC LOW AFFINITY IMMUNOGLOBULIN GAMMA FC  
 CC REGION RECEPTOR II.  
 CC EXTRACELLULAR (POTENTIAL).  
 CC POTENTIAL.  
 CC CYTOPLASMIC (POTENTIAL).  
 CC IG-LIKE C2-TYPE 1.  
 CC IG-LIKE C2-TYPE 2.  
 CC ITIM MOTIF.  
 CC BY SIMILARITY.  
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC ALPGNDPHEMETLPEEVGEYRQPSGGSPVSPGPPSGLE  
 CC PTPSSSPY -> D (in isoform IIB2).  
 CC /FTId=VSP\_002640.  
 CC GEYRQPSGGSPVSPGPPSGLEPTSSPY -> D (in  
 CC isoform IIB1').  
 CC /FTId=VSP\_002641.  
 CC S -> P (IN STRAIN NZB; LY17.1 ALLOTYPED).  
 CC S -> L (IN STRAIN DBA/2; LY17.2  
 CC ALLOTYPED).  
 CC L -> P.

Event=Alternative splicing; N2B; LY17.1 ALLOTYPED; Comment=Additional isoforms seem to exist; Name=C; IsoId=P27645-1; Sequence=Displayed; Name=A; IsoId=P27645-3; Sequence=Not described; Name=B; IsoId=P27645-4; Sequence=Not described; Name=D; IsoId=P27645-5; Sequence=Not described; Name=E; IsoId=P27645-6; Sequence=Not described; Name=F; IsoId=P27645-7; Sequence=Not described; Name=G; IsoId=P27645-8; Sequence=Not described; Name=H; IsoId=P27645-2; Sequence=VSP 002647; TISSUE SPECIFICITY: EXPRESSED ON NATURAL KILLERS CELLS AND MACROPHAGES. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).

EMBL; M64368; AAA42049.1; -  
EMBL; M64369; AAA42048.1; -  
EMBL; M64370; AAA42050.1; -  
EMBL; M32062; AAA41148.1; -  
EMBL; L08446; AAA41151.1; -  
PIR; A35902; A35902.  
PIR; I56110; I56110.  
HSSP; P12319; IALS.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003599; Ig.  
Pfam; PF00047; Ig; 2.  
SMART; SM00409; IG; 2.  
PROSITE; PS50835; IG-LIKE; 2.  
KW IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal; Immunoglobulin domain; Repeat; Alternative splicing.  
FT SIGNAL 1 36  
FT CHAIN 37 267  
FT DOMAIN 37 221  
FT TRANSMEM 222 241  
FT DOMAIN 242 267  
FT DOMAIN 39 121  
FT DOMAIN 122 204  
FT DISULFID 62 104  
FT DISULFID 143 187  
FT VARSPLIC 145 176  
FT VARIANT 36 39  
FT VARIANT 55 55  
FT VARIANT 56 56  
FT VARIANT 115 115  
FT VARIANT 134 134  
FT VARIANT 138 138  
FT VARIANT 184 184  
FT VARIANT 195 195  
FT VARIANT 254 254  
FT SEQUENCE 267 AA; 30281 MW; DD4D6A7A3F70ED92 CRC64;  
Query Match 37.4%; Score 354; DB 1; Length 330;  
Best Local Similarity 41.0%; Pred. No. 3e-24;  
Matches 70; Conservative 32; Mismatches 63; Indels 2; Gaps 2;  
Qy 4 KPKVSLNPPNRIKFNKENTILCNGNPFVESTKWFNG-SLSEETNSLNINAKPED 62  
Db 35 KAVKLEPPPIQVLKEDTTLTCEGPHNPGNSSTQWFHNGRSIRSQVQASYP-KATVND 93  
Qy 63 SGBYKQCHQOVNSEPVILEVSDWLLQLQASAEVWMEGQPLRCHGWRNDDVKVIYK 122  
Db 94 SGEYRCQMEQTRLSDPVGLGVISDWLLLTQPLVLEGETITLRCSHRWKLNIRISFFH 153  
Qy 123 DGEALKWYENHNISTNATVEDSGTYCTGKWOLDVSESPNITV 169  
Db 154 NEXSVRYHYSSNFSIPKANHSGSDYCKSLGRLTHQSPVITV 200  
RESULT 14  
FCG3 RAT  
ID -FCG3\_RAT STANDARD; PRT; 267 AA.  
AC P27645; Q04798; Q63204;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Low affinity immunoglobulin gamma Fc region receptor III precursor  
DE (IgG Fc receptor III) (Fc-gamma RIII) (FCRIII).  
GN FCGR3.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OC NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS B; C AND D).  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=91250730; PubMed=1710249;  
RA Farber D.L., Sears D.W.;  
RT "Rat CD16 is defined by a family of class III Fc gamma receptors requiring co-expression of heteroprotein subunits";  
RN J. Immunol. 146:4352-4361(1991).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RC TISSUE=Natural killer cells;  
RX MEDLINE=90239026; PubMed=1692135;  
RA Zeger D.L., Hogarth P.M., Sears D.W.;  
RT "Characterization and expression of an Fc gamma receptor cDNA cloned from rat natural killer cells";  
RN Proc. Natl. Acad. Sci. U.S.A. 87:3425-3429(1990).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM H).  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RX MEDLINE=93246650; PubMed=8482840;  
RA Farber D.L., Giorda R., Nettleton M.Y., Trucco M., Kochan J.P., Sears D.W.;  
RT "Rat class III Fc gamma receptor isoforms differ in IgG subclass-binding specificity and fail to associate productively with rat CD3 zeta";  
RN J. Immunol. 150:4364-4375(1993).  
CC -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins gamma. Low affinity receptor.  
CC -!- SUBUNIT: MAY FORM MULTISUBUNIT COMPLEX WITH OTHER HETEROPROTEINS. THIS ASSOCIATION IS REQUIRED FOR EFFICIENT CELL-SURFACE EXPRESSION. DOES NOT ASSOCIATE WITH CD3 ZETA.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
Query Match 37.3%; Score 353; DB 1; Length 267;  
Best Local Similarity 41.0%; Pred. No. 2.9e-24;  
Matches 70; Conservative 32; Mismatches 63; Indels 2; Gaps 2;



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Matches 68; Conservative 32; Mismatches 66; Indels 0; Gaps 0;
QY 4 KPVSLNPPNRIKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLNIIVNAKFEDS 63
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 40 KAVKRPDPWIOVLKEDTTLTCEGTHNPGNSSTQFWHQSSTWQVQASVTFKATVND 99
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 GYKCOHQVNESEPVYLEVFDWLLQLQASAEVWEGQLFLRCHGWRNDVVKVIYKD 123
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 100 GEYRCMAHSTSDPVLHLEVISDWLLLPQPLVFEGETITLRCSHWKNKQUTKVLFPQN 159
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 124 GEALKWYENHNISITNAVEDSGTYCTGKWQLDYSEPLNITV 169
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 160 GKPVRYYOSSFIPKANHSHSGNYCYKAYLGRTHWVSKPVTITV 205
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 15
ID FCG3 MOUSE STANDARD; PRT; 261 AA.
AC P08508;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Low affinity immunoglobulin gamma Fc region receptor III precursor
DE (IGG Fc receptor III) (Fc-gamma RIII) (FCRIII).
GN FCGR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87042761; PubMed=2946078;
RA Ravetch J.V., Kuster A.D., Weinshank R., Kochan J., Pavlovic A.,
RA Portnoy D.A., Hulmes J., Pan Y.-C.E., Unkeless J.C.;
RT "Structural heterogeneity and functional domains of murine
RT immunoglobulin G Fc receptors.";
RL Science 234:718-725(1986).
RN [2]
RP SEQUENCE OF 1-29 FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA Soares H.J., Chen M.D., Kulczycki A. Jr.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
CC gamma. Low affinity receptor.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC -----
DR EMBL; M14215; AAA37604.1; -
DR EMBL; X60929; CAA43266.1; -
DR PIR; S29360; S29360.
DR HSSP; P12319; 1ALS.
DR MGD; MGI:95500; Fcgr3.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS00835; IG LIKE; 2.
KW Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW immunoglobulin domain; Repeat.
FT SIGNAL 1 30
FT CHAIN 31 261
FT REGION RECEPTOR III.
FT DOMAIN 31 215
FT TRANSMEM 216 235
FT DOMAIN 236 261
FT CYTOPLASMIC (POTENTIAL).
```

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FT DOMAIN 33 110 IG-LIKE C2-TYPE 1.
FT DOMAIN 116 198 IG-LIKE C2-TYPE 2.
FT DISULFID 56 98 BY SIMILARITY.
FT DISULFID 137 181 BY SIMILARITY.
FT CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 261 AA; 30036 MW; 757PB83668E41069 CRC64;

Query Match 37.2%; Score 352; DB 1; Length 261;
Best Local Similarity 41.3%; Pred. No. 3.4e-24;
Matches 69; Conservative 31; Mismatches 65; Indels 2; Gaps 2;

QY 4 KPVSLNPPNRIKGENVTLTCNGNPFVSTKWFHNGSLSEETNSLNIIVNAKFED 62
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 34 KAVKLPDPWIOVLKEDWVLMCEGTNPGNSSTQFWHNGSIRSQVQASVTF-KATVND 92
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 SGYKCOHQVNESEPVYLEVFDWLLQLQASAEVWEGQLFLRCHGWRNDVVKVIYK 122
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 93 SGYRCQMEQRLSDPVDLGVISDWLLLPQPLVFEGETITLRCSHWKNKLNRIISFFH 152
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 123 DGEALKWYENHNISITNAVEDSGTYCTGKWQLDYSEPLNITV 169
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 153 NEKSVRYHHYKSNFSPKANHSHSGDIYCKSGISGTOHQSKPVTITV 199
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: October 6, 2004, 09:03:39
Job time : 5.81352 secs
```

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:40 ; Search time 27.0629 Seconds  
(without alignments)  
2005.293 Million cell updates/sec

Title: US-10-763-400-13

Perfect score: 947

Sequence: 1 VPQPKVSLNPPWRIKFGK.....GKWQLDYSEPLNITVIKA 172

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_oxganelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	570	60.2	255	6 Q8M130	Q8m130 equus caball
2	561	59.2	260	6 Q8MJ20	Q8mj20 ovis aries
3	376.5	33.8	357	6 Q8SPW5	Q8spw5 macaca fasc
4	371.5	33.2	374	4 Q82663	Q82663 homo sapien
5	371	33.2	280	4 Q82637	Q82637 homo sapien
6	371	33.2	375	4 Q82495	Q82495 homo sapien
7	364.5	33.5	349	6 Q9MZT0	Q9mzt0 bos taurus
8	363.5	33.4	330	11 Q8R142	Q8r142 mus musculus
9	360	33.0	254	6 Q8SPW2	Q8spw2 macaca fasc
10	355	37.5	318	11 Q8V1Q0	Q8v1q0 rattus norv
11	353	37.3	233	4 Q9UPY7	Q9upy7 homo sapien
12	350	37.0	249	11 Q8R477	Q8r477 mus musculus
13	349	36.9	261	11 Q9ES92	Q9es92 mus musculus
14	348.5	36.8	372	6 Q7YQJ5	Q7yqj5 canis famil
15	348	36.7	249	6 Q8N216	Q8n216 felis silve
16	348	36.7	249	11 Q8R2R4	Q8r2r4 mus musculus

17	348	36.7	250	6 Q9N215	Q9n215 felis silve
18	348	36.7	294	6 Q8SPW3	Q8spw3 macaca fasc
19	345	36.4	227	6 Q95N21	Q95n21 mus scrofa
20	345	36.4	256	6 Q95N22	Q95n22 sus scrofa
21	343	36.2	310	6 Q8SPW4	Q8spw4 macaca fasc
22	339	35.8	261	11 Q7TMM9	Q7tmm9 mus musculus
23	339	35.8	316	6 Q8SPV8	Q8spv8 pan troglod
24	332	35.1	316	4 Q8MW64	Q8mw64 homo sapien
25	328	34.6	316	4 Q8WUN1	Q8wun1 homo sapien
26	265	28.0	199	4 Q96P27	Q96p27 homo sapien
27	263	27.8	189	4 Q96P28	Q96p28 homo sapien
28	263	27.8	639	4 Q96P30	Q96p30 homo sapien
29	263	27.8	734	4 Q96P31	Q96p31 homo sapien
30	263	27.8	734	4 Q96LA4	Q96la4 homo sapien
31	263	27.8	740	4 Q96P29	Q96p29 homo sapien
32	263	27.8	742	4 Q8N6S2	Q8n6s2 homo sapien
33	253.5	26.8	582	11 Q8OWN2	Q8own2 mus musculus
34	250	26.4	515	4 Q96RE0	Q96re0 homo sapien
35	247.5	26.1	977	4 Q96RD9	Q96rd9 homo sapien
36	246	26.0	360	4 Q8N732	Q8n732 homo sapien
37	246	26.0	515	4 Q96PJ5	Q96pj5 homo sapien
38	205	21.6	188	4 Q92638	Q92638 homo sapien
39	187.5	19.8	365	4 Q8NEM4	Q8nwm4 homo sapien
40	187.5	19.8	376	4 Q8WXH3	Q8wxh3 homo sapien
41	175.5	18.5	352	11 Q920A9	Q920a9 mus musculus
42	175.5	18.5	353	11 Q8VHP5	Q8vhp5 mus musculus
43	175.5	18.5	353	11 Q8K3U9	Q8k3u9 mus musculus
44	170.5	18.0	509	11 Q91YK7	Q91yk7 mus musculus
45	170.5	18.0	509	11 Q9EQY5	Q9eqy5 mus musculus

#### ALIGNMENTS

RESULT 1

Q8M130 PRELIMINARY; PRT; 255 AA.

AC Q8M130; (T-EMBLrel. 22, Created)

DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (T-EMBLrel. 25, Last annotation update)

DE High affinity immunoglobulin E receptor alpha subunit.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI\_TaxID=9796;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=1; TISSUE=Bronchoalveolar lavage fluid;

RX MEDLINE=20424522; PubMed=10970105;

RA McAleese S.M., Halliwell R.E.W., Miller H.R.P.;

RT "Cloning and Sequencing of the horse and sheep high-affinity IGE

RT receptor alpha chain cDNA."

RL Immunogenetics 51:878-881(2000).

DR GO; GO:0004872; Fireceptor activity; IEA.

DR EMBL; Y18204; CAB40387.1; -.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003598; IG\_c2.

DR Pfam; PF00047; IG; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00408; IGC2; 2.

DR PROSITE; P850835; IG LIKE; 2.

DR Immunoglobulin domain; Receptor.

SQ SEQUENCE 255 AA; 29366 MW; A60659700684FED8 CRC64;

Query Match 60.2%; Score 570; DB 6; Length 255;

Best Local Similarity 62.6%; Pred. No. 4.4e-44;

Matches 109; Conservative 22; Mismatches 39; Indels 4; Gaps 1;

QY 3 QKPKVSLNPPWRIKFGENVITLCGNFFVSSYTKWFNGSLSEETNSLIVAKFED 62

Db 28 RKSTVSLNPPWRIKFGENVITLCGNFFVSSYTKWFNGSLSEETNSLIVAKFED 87

QY 63 SGEYKCOHQVNESEPVYLFVSDWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIYK 122  
 DB 88 SGEYCRNDNLNSAVHLEVFSDWLLQASAEVIEGKALVLCRGKWDVFKVIYK 147  
 QY 123 DGEALKYWNHNISITNATVEDSGTYCTG-----KWQLDYSEPLNITVIKA 172  
 DB 148 DGKPLEYWNKNISIESATTENSCTYCEGAFNFKRTSERYTSDYLNITVIKKA 201

## RESULT 2

Q8MJZO PRELIMINARY; PRT; 260 AA.  
 AC Q8MJZO;  
 DT 01-OCT-2002 (TREMELrel. 22, Created)  
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE High affinity immunoglobulin E receptor alpha subunit.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1; TISSUE=Bone marrow;  
 RX MEDLINE=20424522; PubMed=10970105;  
 RA McAleese S.M., Halliwell R.E.W., Miller H.R.P.;  
 RT "Cloning and Sequencing of the horse and sheep high-affinity IGE  
 receptor alpha chain cDNA".  
 RL Immunogenetics 51:878-891(2000).  
 DR EMBL; Y18205; CAB40544.1; -.  
 DR GO; GO:0004872; Fireceptor activity; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00408; IGC2; 2.  
 DR PROSITE; PSS0835; IG\_LIKE; 2.  
 KW Immunoglobulin domain; Receptor.  
 SQ SEQUENCE 260 AA; 30047 MW; 67111F2F17D596ED CRC64;

Query Match 59.2%; Score 561; DB 6; Length 260;

Best Local Similarity 61.3%; Pred. No. 3e-43; Indels 0; Gaps 0;  
 Matches 103; Conservative 21; Mismatches 44;

QY 4 KPKVSLNPPNRRIFKGNVTLTCNGNFFEVSTKWFHNGSLSEETNSLNIVNAKFDS 63  
 DB 30 KSKVSLNPPNRRIFRGTETVTLTCGVNRSSESSVHNGTTLKETNSRWDIVKRVQDS 89  
 QY 64 GEYKCOHQVNESEPVYLFVSDWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIYK 123  
 DB 90 GKYYCRKGFASPEVYLVNVDWLLQASAEVVMGEGSLFLRCHSKNKNLAFKVIYK 149  
 QY 124 GEALKYWNHNISITNATVEDSGTYCTGKQVQLDYSEPLNITVIK 171  
 DB 150 NRALKYWNHNISITNATVEDSGTYCTGKQVQLDYSEPLNITVIK 197

## RESULT 3

Q8SPW5 PRELIMINARY; PRT; 357 AA.  
 AC Q8SPW5;  
 DT 01-JUN-2002 (TREMELrel. 21, Created)  
 DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE FC gamma receptor I.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Macaca.

OX NCBI\_TaxID=9541;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Namenuk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,  
 RA Presta L.G.;  
 RT "Binding of human IgG to cynomolgus FcR";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF489812; AAL92095.1; -.  
 DR GO; GO:0004872; Fireceptor activity; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00409; IG; 3.  
 DR PROSITE; PSS0835; IG\_LIKE; 3.  
 KW Receptor.  
 SQ SEQUENCE 357 AA; 40715 MW; F5C51A06A3BCB08F CRC64;

Query Match 39.8%; Score 376.5; DB 6; Length 357;

Best Local Similarity 41.0%; Pred. No. 3.1e-26;  
 Matches 68; Conservative 36; Mismatches 61; Indels 1; Gaps 1;

QY 4 KPKVSLNPPNRRIFKGNVTLTCNGNFFEVSTKWFHNGSLSEETNSLNIVNAKFDS 63  
 DB 21 KAVITLQPPWVSFQETVTLQCEVPRLPGSSSTQWFLNGTATQTSTPSRYTSASVKDS 80  
 QY 64 GEYKCOHQVNESEPVYLFVSDWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIYK 123  
 DB 81 GEYRCQRGSGSDPIQLSHRDWLLQVSSRVFTEGEPLALRCHAWKDLVYNVLYQN 140  
 QY 124 GEALKYWNHNISITNATVEDSGTYCTGKQVQLDYSEPLNITV 169  
 DB 141 GKAFKFFYRNSQLTKTNISHNGAYHCSG-MGKHRYTSAGVSVTV 185

## RESULT 4

Q92663 PRELIMINARY; PRT; 374 AA.  
 AC Q92663;  
 DT 01-FEB-1997 (TREMELrel. 02, Created)  
 DT 01-FEB-1997 (TREMELrel. 02, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE FC gamma receptor I.  
 GN AI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=93055454; PubMed=1430234;  
 RA Porges A.J., Redecha P.B., Doebele R., Pan L.C., Salmon J.E.,  
 RA Kimberly R.P.;  
 RT "Novel FC gamma receptor I family gene products in human mononuclear  
 cells";  
 RL J. Clin. Invest. 90:2102-2109(1992).  
 DR EMBL; L03418; AAA36049.1; -.  
 DR PIR; A39878; A39878.  
 DR GO; GO:0004872; Fireceptor activity; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00408; IGC2; 1.  
 DR PROSITE; PSS0835; IG\_LIKE; 3.  
 KW Immunoglobulin domain; Receptor.  
 SQ SEQUENCE 374 AA; 42632 MW; D33D59398CEA699 CRC64;

Query Match 39.2%; Score 371.5; DB 4; Length 374;

Best Local Similarity 41.0%; Pred. No. 9.5e-26;  
 Matches 68; Conservative 37; Mismatches 60; Indels 1; Gaps 1;

QY 4 KPKVSLNPPNRRIFKGNVTLTCNGNFFEVSTKWFHNGSLSEETNSLNIVNAKFDS 63

Db 21 KAVITLQPPWVSFQEEVTLHCEVHLPGSSSTQWFLNGTATQTSTPSYRITSASVND 80  
Qy 64 GEYKCOHQVNESEPVLYEVSDMLLQASAEVWMEGQPLFLRCHGWRNMDVYKVIYKD 123  
Db 81 GEYRCQGLSGRSDPIQLIEHGRWLLQLQVSSRVFTEGEPLALRCHAWKDKLVNVLVYRN 140  
Qy 124 GEALKYWEHNISITNATVDSGTYYCTGKQVWQLDYSEPLNLT 169  
Db 141 GRAKFFHNSNLTKTNISHNGTYHCSG-MGKHRYTSAGISVT 185

RESULT 5  
Q92637 ID Q92637 PRELIMINARY; PRT; 280 AA.  
AC Q92637;  
DT 01-FEB-1997 (TRENBLrel. 02, Created)  
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE FC gamma receptor I.  
GN B1  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood.  
RA Forges A.J., Redecha P.B., Dosebele R., Pan L.C., Salmon J.E.,  
RA Kimberly R.P.;  
RT "Novel Fc gamma receptor I family gene products in human mononuclear  
RT cells";  
RL J. Clin. Invest. 90:2102-2109(1992).  
DR EMBL; L03419; AAA35825.1; -.  
DR PIR; I55577; I55577.  
DR GO; GO:0005886; C:plasma membrane; NAS.  
DR GO; GO:0003793; F:defense/immunity protein activity; NAS.  
DR GO; GO:0016489; F:immunoglobulin receptor activity; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR Pfam; PF00047; IG; 2.  
DR SMART; SM00409; IG; 2.  
DR PROSITE; PS50835; IG\_LIKE; 2.  
KW Receptor.  
SQ SEQUENCE 280 AA; 32232 MW; C6C6C45AE3D345C6 CRC64;

Query Match 39.2%; Score 371; DB 4; Length 280;  
Best Local Similarity 43.3%; Pred. No. 7.3e-26;  
Matches 65; Conservative 32; Mismatches 53; Indels 0; Gaps 0;  
Qy 4 KPKVSLNPPWNRIFKGNVTLTCGNFFVSTKWFHNGSLSEETNSLNIVNAKPEDS 63  
Db 21 KAVITLQPPWVSFQEEVTLHCEVHLPGSSSTQWFLNGTATQTSTPSYRITSASVND 80  
Qy 64 GEYKCOHQVNESEPVLYEVSDMLLQASAEVWMEGQPLFLRCHGWRNMDVYKVIYKD 123  
Db 81 GEYRCQGLSGRSDPIQLIEHGRWLLQLQVSSRVFTEGEPLALRCHAWKDKLVNVLVYRN 140  
Qy 124 GEALKYWEHNISITNATVDSGTYYCTG 153  
Db 141 GRAKFFHNSNLTKTNISHNGTYHCSG 170

RESULT 6  
Q92495 ID Q92495 PRELIMINARY; PRT; 375 AA.  
AC Q92495;  
DT 01-FEB-1997 (TRENBLrel. 02, Created)  
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE FC gamma receptor type I (Fc gamma RIB=Fc gamma receptor).

GN CD64 OR FC-GAMMA>RIB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood.  
RA Benesh P.D., Sastry K.N., Iyer R.R., Eichbaum Q.G., Raveh D.,  
RA Ezekowitz A.B.;  
RL Submitted (DEC-1992) to the EMBL/GenBank/DBSJ databases.  
RN [2]  
RP SEQUENCE OF 1-224 FROM N.A.  
RX MEDLINE=93018827; PubMed=1402657;  
RA Benesh P.D., Sastry K., Iyer R.R., Eichbaum Q.G., Raveh D.P.,  
RA Ezekowitz R.A.;  
RT "Definition of interferon gamma-response elements in a novel human Fc  
RT gamma receptor gene (Fc gamma RIB) and characterization of the gene  
RT structure";  
RL J. Exp. Med. 176:1115-1123(1992).  
DR EMBL; M91555; AAA58414.1; -.  
DR EMBL; M91550; AAA58414.1; JOINED.  
DR EMBL; M91551; AAA58414.1; JOINED.  
DR EMBL; M91552; AAA58414.1; JOINED.  
DR EMBL; M91553; AAA58414.1; JOINED.  
DR EMBL; M91554; AAA58414.1; JOINED.  
DR EMBL; M91555; AAA58414.1; JOINED.  
DR EMBL; S45709; AAD13842.1; -.  
DR EMBL; S45707; AAD13842.1; JOINED.  
DR EMBL; S45708; AAD13842.1; JOINED.  
DR EMBL; S45704; AAD13842.1; JOINED.  
DR EMBL; S45705; AAD13842.1; JOINED.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003598; IG\_c2.  
DR Pfam; PF00047; IG; 3.  
DR SMART; SM00408; IGC2; 1.  
DR PROSITE; PS50835; IG\_LIKE; 3.  
KW Immunoglobulin domain.  
SQ SEQUENCE 375 AA; 42881 MW; A84D464C70DD0F91 CRC64;

Query Match 39.2%; Score 371; DB 4; Length 375;  
Best Local Similarity 43.3%; Pred. No. 1.1e-25;  
Matches 65; Conservative 32; Mismatches 53; Indels 0; Gaps 0;  
Qy 4 KPKVSLNPPWNRIFKGNVTLTCGNFFVSTKWFHNGSLSEETNSLNIVNAKPEDS 63  
Db 21 KAVITLQPPWVSFQEEVTLHCEVHLPGSSSTQWFLNGTATQTSTPSYRITSASVND 80  
Qy 64 GEYKCOHQVNESEPVLYEVSDMLLQASAEVWMEGQPLFLRCHGWRNMDVYKVIYKD 123  
Db 81 GEYRCQGLSGRSDPIQLIEHGRWLLQLQVSSRVFTEGEPLALRCHAWKDKLVNVLVYRN 140  
Qy 124 GEALKYWEHNISITNATVDSGTYYCTG 153  
Db 141 GRAKFFHNSNLTKTNISHNGTYHCSG 170

RESULT 7  
Q9WZT0 ID Q9WZT0 PRELIMINARY; PRT; 349 AA.  
AC Q9WZT0;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE FC gamma receptor I.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20349800; PubMed=10889306;  
RA Yan Y., Li X., Wang A., Zhang G.;

RT "Molecular cloning and identification of full-length cDNA encoding  
 RT high affinity Fc receptor for bovine IgG (Fc gamma RI).";  
 RL Vet. Immunol. Immunopathol. 75:151-159(2000).

DR EMBL; AF162866; AAF80477.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00408; Igc2; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR Immunoglobulin domain; Receptor.  
 KW SEQUENCE 349 AA; 39608 MW; D0B77B2EP9408C02 CRC64;

Query Match 38.5%; Score 364.5; DB 6; Length 349;  
 Best Local Similarity 41.1%; Pred. No. 3.8e-25;  
 Matches 69; Conservative 36; Mismatches 62; Indels 1; Gaps 1;

QY 2 PQKQVSLNPPNRRIFKGNVTLCNGNNFFVSTKWFHNGSLSEETNSLNVNAKFE 61  
 Db 19 PTKAVITLKPWVSVFQENVTLLCGEPHPCGTATQWFLNGTAKTLAPRYSINSATFD 78  
 QY 62 DSGEYKQHQVNESEPVYLEVFDWLLLOASAEVWEGQPLFLRCHGRWWDVYKVIY 121  
 Db 79 DSGEYKQGLSMDPVLQVLEHSDWLLLTQVSRVFTGDPALRCHGRWWDVYKVIY 138  
 QY 122 KDGEALKYVNHENISITNATVEDSGTYCTGKVMQLDYSEPLNITV 169  
 Db 139 KDGKPRFSSQSDSETILTQNLSHNGIYHCSE-RRRYTSAGVSITI 185

## RESULT 8

Q8R142 PRELIMINARY; PRT; 330 AA.

AC Q8R142; (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DE Hypothetical protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1];  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC025535; AAH25535.1; -.  
 DR InterPro; IPR007110; IG-LIKE.  
 DR InterPro; IPR003598; IG\_c2.  
 DR Pfam; PF00047; ig; 3.  
 DR SMART; SM00408; Igc2; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 KW Hypothetical protein; Immunoglobulin domain.  
 FT NON\_TER  
 SQ SEQUENCE 330 AA; 37116 MW; 891F8724F870D8BE CRC64;

Query Match 38.4%; Score 363.5; DB 11; Length 330;  
 Best Local Similarity 44.3%; Pred. No. 4.4e-25;  
 Matches 74; Conservative 33; Mismatches 57; Indels 3; Gaps 3;

QY 4 KPKVSLNPPNRRIFKGNVTLCNGNNFFVSTKWFHNGSLSEETNSLNVNAKFE 63  
 Db 25 KAVITLQPPWASIFQKENVTLWCCEPHLPDGSSTQFWINGIVTSTPSYISVASQDS 84  
 QY 64 GYKQHQVNESEPVYLEVFDWLLLOASAEVWEGQPLFLRCHGRWWDVYKVIY 122  
 Db 85 GEYRQIGSVSDPVLQVLEHSDWLLLTQVSRVFTGDPALRCHGRWWDVYKVIY 144  
 QY 123 DGEALKYVNHENISITNATVEDSGTYCTGKVMQLDYSEPLNITV 169  
 Db 145 NGRSKF-SGSKIALKTLNLSHNGIYHCSE-MGRHYTSAGVSITI 189

## RESULT 9

Q8SPW2 PRELIMINARY; PRT; 254 AA.

AC Q8SPW2; (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Fc gamma receptor IIIfa.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
 OC Cercopitheidae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1];

SEQUENCE FROM N.A.

RP TISSUE=Spleen;  
 RC Namenuk A.K.; Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,  
 RA Presta L.G.;  
 RL "Binding of human IgG to cynomolgus FcR.";  
 RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF485815; AAL92098.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 KW Receptor.  
 SQ SEQUENCE 254 AA; 29120 MW; 11A486B3A34AF7B CRC64;

Query Match 38.0%; Score 360; DB 6; Length 254;  
 Best Local Similarity 42.8%; Pred. No. 6.6e-25;  
 Matches 71; Conservative 29; Mismatches 66; Indels 0; Gaps 0;

QY 4 KPKVSLNPPNRRIFKGNVTLCNGNNFFVSTKWFHNGSLSEETNSLNVNAKFE 63  
 Db 25 KAVITLQPPWVLEKDRVTLKCGAYSPEDNSTWFWHNSLISSOTSYFAAARVNS 84  
 QY 64 GEYKQHQVNESEPVYLEVFDWLLLOASAEVWEGQPLFLRCHGRWWDVYKVIY 123  
 Db 85 GEYRQIGSVSDPVLQVLEHSDWLLLTQVSRVFTGDPALRCHGRWWDVYKVIY 144  
 QY 124 GEALKYVNHENISITNATVEDSGTYCTGKVMQLDYSEPLNITV 169  
 Db 145 GKGRKYFHQNSDFYIPKALDKSGSYFCGLIGSKXNSSETVNI 190

## RESULT 10

Q8VIOQ PRELIMINARY; PRT; 318 AA.

AC Q8VIOQ; (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Fc gamma receptor II beta (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1];

SEQUENCE FROM N.A.

RP STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RC Even J., Jouvin-Marche E., Hogarth P.M., Cazenave P.-A.;  
 RT "DNA and protein polymorphism of murid Fc gamma receptor II.";  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; M33710; AAL29888.1; -.  
 DR EMBL; M33707; AAL29888.1; JOINED.  
 DR EMBL; M33708; AAL29888.1; JOINED.  
 DR EMBL; M33709; AAL29888.1; JOINED.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR Pfam; PF00047; ig; 4.

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DR SMART; SM00409; IG; 3.
KW PROSITE; PS50835; IG_LIKE; 4.
FT NON_TER 318 318
SQ SEQUENCE 318 AA; 36270 MW; 1E088142F2B4A4E CRC64;
Query Match 37.5%; Score 355; DB 11; Length 318;
Best Local Similarity 40.4%; Pred. NO. 2.5e-24;
Matches 67; Conservative 32; Mismatches 67; Indels 0; Gaps 0;
QY 4 KPKVSLNPPNRIKFGENVLTTCGNFFVSSYTKWPHNGSLSEETNSLNIVNAKPEDS 63
Db 151 KAVKLEPWPQVLKEDVTLMCEGHTNKKCSQWPHNGSSIHQAQANTFTKATVND 210
QY 64 GEYKCOHQVNESEPVYLEVFSDFWLLLOAASAEVVMGQPLFLRCHGRWNRWDVYKVIYKD 123
Db 211 GEYRCLMEETGISEPIHLGVISDWLLLOTSQVLEEGETITLRSCHSKNKLTKVLLFQN 270
QY 124 GEALKYWNENISITNATVEDSGTYCTGKWQLDYSEPLNITV 169
Db 271 GKPVRYHQSNFSPKANHSNGYCKAYGLRTHMVSKEVTITV 316
RESULT 11
Q9UPV7
ID Q9UPY7 PRELIMINARY; PRT; 233 AA.
AC Q9UPY7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE FC-gamma receptor IIIB (CD 16).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20487377; PubMed=11034564;
RA Katanabe Y., Shinada E., Fujiwara K., Niihara H., Shimano K.,
RA Mitsunaga S., Tadokoro K., Jui T.;
RT "Nucleotide sequence of a new Fc gamma receptor IIIB allele that codes
RT for a neutrophil antigen.";
RL Tissue Antigens 56:272-275(2000).
DR EMBL; AB025256; BAA81803.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
KW RECEPTOR.
FT VARIANT 54 54 K -> E.
SQ SEQUENCE 233 AA; 26215 MW; 74B51B909272B388 CRC64;
Query Match 37.3%; Score 353; DB 4; Length 233;
Best Local Similarity 43.4%; Pred. NO. 2.6e-24;
Matches 72; Conservative 26; Mismatches 68; Indels 0; Gaps 0;
QY 4 KPKVSLNPPNRIKFGENVLTTCGNFFVSSYTKWPHNGSLSEETNSLNIVNAKPEDS 63
Db 25 KAVVLEPQWVLEKDSVTLKCCQAGSPKDNSTQWFHNSLSLSSQASSYFIDAATVND 84
QY 64 GEYKCOHQVNESEPVYLEVFSDFWLLLOAASAEVVMGQPLFLRCHGRWNRWDVYKVIYKD 123
Db 85 GEYRCLNLSLSPVQVLEHIGWLLLOAARWVFEEDPHLRCHSKWNTALHKVYLQN 144
QY 124 GEALKYWNENISITNATVEDSGTYCTGKWQLDYSEPLNITV 169
Db 145 GKDRKYFHNSDFHPIKATLKDSGYFCRGLGVSKNVSSTVNIIT 190
RESULT 12
Q8R477
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ID Q8R477 PRELIMINARY; PRT; 249 AA.
AC Q8R477;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transmembrane receptor CD16-2.
GN FCRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RA Mechetina L.V., Najakshin A.M., Alabyev B.Y., Chikaev N.A.,
RA Tarantin A.V.;
RT "Identification of CD16-2, a novel mouse receptor homologous to
RT CD16/FCGR111.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF49613; AAM19249.1; -.
DR MGD; MGI:2179523; Fcrl3.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW RECEPTOR.
SQ SEQUENCE 249 AA; 28382 MW; 3DEAF3D935BEP5CD CRC64;
Query Match 37.0%; Score 350; DB 11; Length 249;
Best Local Similarity 41.3%; Pred. NO. 5.2e-24;
Matches 69; Conservative 31; Mismatches 67; Indels 0; Gaps 0;
QY 3 QKPKVSLNPPNRIKFGENVLTTCGNFFVSSYTKWPHNGSLSEETNSLNIVNAKPED 62
Db 23 QKAVNLDPKWTVLEEDSVTLRCQGFSPEDNSIKWFHNSLIHQDANYVIQSAVKD 82
QY 63 SGEYKCOHQVNESEPVYLEVFSDFWLLLOAASAEVVMGQPLFLRCHGRWNRWDVYKVIYK 122
Db 83 SGMYRCQTALSTISDPVQVLEHVMGWLLOTTKWLQEGDPIHLRCHSMQNRPRVKVYLYQ 142
QY 123 DGEALKYWNENISITNATVEDSGTYCTGKWQLDYSEPLNITV 169
Db 143 NGKGRKYFHENSELPIPKATHNDSGSYFCRGLIGHNNKSSASFRISL 189
RESULT 13
Q9ES92
ID Q9ES92 PRELIMINARY; PRT; 261 AA.
AC Q9ES92;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fc gamma receptor III.
GN FCGR3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Fossati Jimack L., Boucrot E., Izui S.;
RT "Mouse Fc gamma RIIB: identification and characterization of a new
RT allele in C57BL/6 mice.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
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"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."

RT Nature 420:563-573(2002).  
 RL EMBL; AF197930; AAC28520.1; -  
 DR EMBL; AK072227; BAC36696.1; -  
 DR MGB; WGI:95500; Fcgr3.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 KW Receptor.  
 SQ SEQUENCE 261 AA; 30098 MW; 9C8570E032F94730 CRC64;

Query Match 36.9%; Score 349; DB 11; Length 261;  
 Best Local Similarity 41.3%; Pred. No. 6.9e-24;  
 Matches 69; Conservative 30; Mismatches 66; Indels 2; Gaps 2;

QY 4 KPKYSLNPPNRI FKGNVTLTCGNFFVSVSTKWFHN-GSLSETRSSLNIVNAKTED 62  
 Db 34 KAVVLEPPNRI FKGNVTLTCGNFFVSVSTKWFHN-GSLSETRSSLNIVNAKTED 62  
 QY 63 SGEYKCOHQVNESEPVYLEVFDWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIYK 122  
 Db 93 SGEYRCQEQRLSDPDVLCVSDWLLQTPQRFLEGETITLRCHSWENKLNRIISFFH 152  
 QY 123 DGEALKYWNHNISITNATVEDSGTYCTGKQWLDYSEPLNITY 169  
 Db 153 NEKSVRVHYHNSIPKXANHSBGDYCKGSLGSGTQHSKQVPTIV 199

RESULT 14  
 QYQJ5 PRELIMINARY; PRT; 372 AA.  
 ID QYQJ5  
 AC QYQJ5  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE High affinity IgG Fc gamma receptor 1.  
 GN FCGAMMARI.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Shiba; TISSUE=Cutaneous;  
 RX MEDLINE=22777889; PubMed=12811428;  
 RA Nakamura R., Sato Y., Takagi K., Sasaki N., Sawada J., Kitani S.,  
 RA Teshima R.  
 RT "Presence and primary sequence of a high-affinity IgG receptor on  
 canine mastocytoma (GM-MC) cells."  
 RL Immunogenetics 55:271-274(2003).  
 DR EMBL; AB101519; BAC80263.1; -  
 KW Receptor.  
 SQ SEQUENCE 372 AA; 42336 MW; BC04026CD198049D CRC64;

Query Match 36.8%; Score 348.5; DB 6; Length 372;  
 Best Local Similarity 39.3%; Pred. No. 1.2e-23;  
 Matches 67; Conservative 33; Mismatches 67; Indels 1; Gaps 1;

QY 2 POKPVSLNPPNRI FKGNVTLTCGNFFVSVSTKWFHNGSLSETRSSLNIVNAKFE 61  
 Db 19 PVKAVITLQPPVSVFQESVTLWCPEGPHLPGLSDSTQWFLNGTATQTLTPYRIAAASVN 78  
 QY 62 DSGEYKCOHQVNESEPVYLEVFDWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIY 121  
 Db 79 DNGEYRCQGLSVLSDFIQLGHDRDILLQVSGRVFTEGEPTLRCHGWRNKLNVNLFY 138  
 QY 122 KDGEALKYWNHNISITNATVEDSGTYCTGKQWLDYSEPLNITY 169  
 Db 139 QNGTVLKFPSPNSEFTILKTLHNGIYHCSA-MGKHYESAGVSITI 185

## RESULT 15

Q9N2I6 PRELIMINARY; PRT; 249 AA.  
 ID Q9N2I6

AC Q9N2I6  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE CD16.  
 GN CD16.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20180233; PubMed=10713347;  
 RX Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,  
 RA Mikami T., Takahashi B.;  
 RT "Molecular cloning and sequencing of the cDNA encoding the feline  
 Fc(gamma)RIIIA (CD16) homologue";  
 RL Vet. Immunol. Immunopathol. 73:353-359(2000).  
 DR EMBL; AB025314; BAA92347.1; -  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IG; 2.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 SQ SEQUENCE 249 AA; 27902 MW; 683528C68A7CAB7A CRC64;

Query Match 36.7%; Score 348; DB 6; Length 249;  
 Best Local Similarity 42.8%; Pred. No. 8e-24;  
 Matches 71; Conservative 25; Mismatches 70; Indels 0; Gaps 0;

QY 4 KPKVSLNPPNRI FKGNVTLTCGNFFVSVSTKWFHNGSLSETRSSLNIVNAKTEDS 63  
 Db 24 KAVVLEPPNRI FKGNVTLTCGNFFVSVSTKWFHNGSLSETRSSLNIVNAKTEDS 83  
 QY 64 GEYKCOHQVNESEPVYLEVFDWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIYKD 123  
 Db 84 GEYKCOHQVNESEPVYLEVFDWLLQASAEVVMGQPLFLRCHGWRNWDVYKVIYKD 143  
 QY 124 GEALKYWNHNISITNATVEDSGTYCTGKQWLDYSEPLNITY 169  
 Db 144 GRGKMFHKNDFIYIPKATSKHSGSYFCRGLIGNKNSSEAVNITY 189

Search completed: October 6, 2004, 09:07:04  
 Job time : 28.0629 secs